

CC This invention describes a novel use of bromelain proteases (I) for
 CC the treatment of diarrhoea and other conditions caused by bacteria, but
 CC inhibit both formation of fibrin and adhesion of thrombocytes to
 CC endothelial cells. (I) are about 10 times more active than bromelain
 CC and are used in the treatment of diarrhoea and other conditions
 CC present bromelain proteases isolated from pineapple (Ananas comosus)
 CC which are used in the method of the invention.

XX Sequence 20 AA:
 Query Match Similarity 100.0%; Score 108; DB 21; Length 20;
 Mismatches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQSDIMRDYGATVSVNQN 20
 DB 1 VPQSDIMRDYGATVSVNQN 20
 RESULT 2
 ID AAK87550 standard; protein; 213 AA.
 XX AAK87550;
 XX AAK87550;
 DT 18-JUN-1994 (first entry)
 DB Stem bromelain protease.
 XX Enzyme, esp. bromelain, contn. compn. for control of diarrhoea;
 XX proteolytic enzyme, cysteine protease; diarrhoea, fluid secretion;
 XX gastro-intestinal tract; GI tract; absorption.
 XX Ananas comosus.
 XX M09400147-A.
 XX 06-JAN-1994.
 XX 30-JUN-1993; 93NC-GM01374.
 XX PR 30-JUN-1992; 92GB-001862.
 XX PR 30-JUN-1992; 92GB-001864.
 XX PR 25-JUN-1993; 93GB-001388.
 XX PR 25-JUN-1993; 93GB-001388.
 XX (CORT-) CORTECS LTD.
 XX Mynot TL;
 XX WPI; 1994-025889/03.
 XX WPI; 1994-025889/03.
 PT Enzyme, esp. bromelain, contn. compn. for control of diarrhoea -
 PT inhibits fluid secretion in the gut and promotes absorption
 XX Diactoneur, Page 11-13; 70pp; English.
 CC The sequence is that of stem bromelain protease, a mature of
 CC protein is a cysteine protease used to treat infectious diarrhoea
 CC caused by heat labile or heat stable toxins, enterotoxigenic E. coli
 CC inhibits the secretory effect of the toxins and prevents attachment
 CC of bacteria to the intestinal lining. It also inhibits secretion
 CC of bacteria to the intestinal lining. It also inhibits secretion
 CC of bacteria to the intestinal lining. It also inhibits secretion
 CC adverse effect on nutrient influx.
 XX Sequence 213 AA;
 Query Match Similarity 100.0%; Score 108; DB 15; Length 213;
 Mismatches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQSDIMRDYGATVSVNQN 20

DB 2 VPQSDIMRDYGATVSVNQN 21
 RESULT 3
 ID AAK68974 standard; protein; 213 AA.
 XX AAK68974;
 XX AAK68974;
 DT 09-AUG-1995 (first entry)
 DB Pineapple stem bromelain protease.
 XX Enzyme, esp. bromelain, contn. compn. for control of diarrhoea;
 XX proteolytic enzyme, cysteine protease; diarrhoea, fluid secretion;
 XX gastro-intestinal tract; GI tract; absorption.
 XX Ananas comosus.
 XX M09500169-A.
 XX 05-JAN-1995.
 XX 24-JUN-1994; 94NC-GM01368.
 XX PR 25-JUN-1993; 93GB-001388.
 XX PR 25-JUN-1993; 93GB-001388.
 XX (CORT-) CORTECS LTD.
 XX Mynot TL;
 XX WPI; 1995-051751/07.
 XX WPI; 1995-051751/07.
 PT Enzyme, esp. bromelain, contn. compn. for control of diarrhoea -
 PT dependent on cyclic nucleotide pathways e.g. cholera, diphtheria
 XX or cancer
 XX Claim 1; Page 35; 45pp; English.
 CC Pineapple stem bromelain protease is used in the treatment of
 CC prophylaxis of conditions which are dependent on cyclic nucleotide
 CC and other intracellular and/or extracellular pathways. The diseases
 CC include cholera, diphtheria, and other infectious diseases. The
 CC infections such as cholera, diphtheria and pertussis.
 XX Sequence 213 AA;
 Query Match Similarity 100.0%; Score 108; DB 16; Length 213;
 Mismatches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQSDIMRDYGATVSVNQN 20
 DB 2 VPQSDIMRDYGATVSVNQN 21
 RESULT 4
 ID AAK83105 standard; Protein; 311 AA.
 XX AAK83105;
 XX AAK83105;
 DT 04-JUL-2000 (first entry)
 DB 710 Protease from pineapple stem.
 XX Protease, pineapple, treatment, prevention, prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX immunosuppressant; immunodeficiency; HIV; immunisation; trauma, burn,
 XX surgery; genetic abnormality; diabetes; nitric oxide; NO;
 XX anti-infectious.

CC Acanas comensis.
 PM M0200014353-AL.
 XX 16-MAR-2000.
 PF 24-AUG-1999; 99NC-0802784.
 PR 02-SEP-1998; 98GB-0019138.
 XX (CORT-) CORTCS UK LTD.
 XX Wymott TL, Crockett B;
 PI WPI: 2000-26598/22.
 DR N-P8DB; RA23391.
 XX Stem bromelain-like proteinases useful for the prevention and treatment
 PT of cancer and diseases or conditions which respond to increased nitric
 PT oxide production are encoded by nucleic acid sequences isolated from a
 PT pineapple stem -
 XX Claim 4; Page 58-59; 72pp; English.
 PS
 XX The sequences encoding proteinases from pineapple stem have
 CC the same activity as a stem bromelain-like proteinase, CCX2.
 CC The proteinases can be used in human or veterinary medicine and
 CC also be used as an immunomodulant or in the preparation of an
 CC non-solid tumours and virus induced tumours. The proteinases can
 CC also be used as an immunomodulant or in the preparation of an
 CC malnutrition, infection (e.g. HIV and malaria), tumours (e.g.
 CC lymphoid, myeloid), trauma (e.g. burns, wounds, surgery) medical
 CC treatment (e.g. with drugs such as steroids, cyclosporin and
 CC cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
 CC genetic abnormalities (e.g. in combined immunodeficiency patients
 CC lacking B or T cells), diabetes and old age. The proteinase can
 CC be used in the treatment or prevention of disease cases can
 CC conditions which respond to increased nitric oxide (NO) production,
 CC or as an antimicrobial agent or the component of an antimicrobial
 CC agent.
 XX
 SQ Sequence 311 AA;
 Query Match 91.7%; Score 99; DB 21; Length 311;
 Best Local Similarity 90.0%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OV 1 VPQSDIMDVGATGVYXN 20
 DB 96 VPQSDIMDVGATGVYXN 115
 RESUME 5
 ID ANY83107 standard; Protein: 324 AA.
 XX
 XX ANY83107;
 XX 04-JUL-2000 (first entry)
 DB D88686 proteinase from pineapple stem.
 XX Proteinase, pineapple, pineapple, prevention, prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX immunomodulant; immunodeficiency; HIV; malaria; tumours (e.g.
 XX lymphoid, myeloid); trauma (e.g. burns, wounds, surgery, burn,
 XX surgery); genetic abnormalities; diabetes; nitric oxide; NO;
 XX antimicrobial.
 XX Acanas comensis.
 PM M0200014353-AL.
 XX

XX 16-MAR-2000.
 XX 24-AUG-1999; 99NC-0802784.
 PR 02-SEP-1998; 98GB-0019138.
 XX (CORT-) CORTCS UK LTD.
 XX Wymott TL, Crockett B;
 PI WPI: 2000-26598/22.
 DR N-P8DB; RA23391.
 XX Stem bromelain-like proteinases useful for the prevention and treatment
 PT of cancer and diseases or conditions which respond to increased nitric
 PT oxide production are encoded by nucleic acid sequences isolated from a
 PT pineapple stem -
 XX Claim 4; Page 64-66; 72pp; English.
 PS
 XX The sequences encoding proteinases from pineapple stem have
 CC the same activity as a stem bromelain-like proteinase, CCX2.
 CC The proteinases can be used in human or veterinary medicine and
 CC also be used as an immunomodulant or in the preparation of an
 CC non-solid tumours and virus induced tumours. The proteinases can
 CC also be used as an immunomodulant or in the preparation of an
 CC malnutrition, infection (e.g. HIV and malaria), tumours (e.g.
 CC lymphoid, myeloid), trauma (e.g. burns, wounds, surgery) medical
 CC cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
 CC genetic abnormalities (e.g. in combined immunodeficiency patients
 CC lacking B or T cells), diabetes and old age. The proteinase can
 CC be used in the treatment or prevention of disease cases can
 CC conditions which respond to increased nitric oxide (NO) production,
 CC or as an antimicrobial agent or the component of an antimicrobial
 CC agent.
 XX
 SQ Sequence 324 AA;
 Query Match 91.7%; Score 99; DB 21; Length 324;
 Best Local Similarity 90.0%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OV 1 VPQSDIMDVGATGVYXN 20
 DB 96 VPQSDIMDVGATGVYXN 115
 RESUME 6
 ID ANY83104 standard; Protein: 351 AA.
 XX
 XX ANY83104;
 XX 04-JUL-2000 (first entry)
 DB 674 proteinase from pineapple stem.
 XX Proteinase, pineapple, pineapple, prevention, prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX immunomodulant; immunodeficiency; HIV; malaria; tumours (e.g.
 XX lymphoid, myeloid); trauma (e.g. burns, wounds, surgery, burn,
 XX surgery); genetic abnormalities; diabetes; nitric oxide; NO;
 XX antimicrobial.
 XX Acanas comensis.
 PM M0200014353-AL.
 XX 16-MAR-2000.
 XX

PA (CORT-) CORTECS UK LTD.
 XX
 PA Myocot TL, Crosseatt B;
 XX
 DB WP1: 2000-265998/22.
 XX
 DB N-PSDB: AA293182.
 XX
 PR Stem bromelain-like proteinases useful for the prevention and treatment
 PR of cancer and diseases of condition which respond to increased nitric
 PR oxide production are encoded by nucleic acid sequences isolated from a
 PR pineapple stem -
 XX
 XX
 XX Claim 4: Page 44-51: 72pp: English.
 XX
 XX The sequence encoding proteinases from pineapple stem have
 XX the same activity as a stem bromelain-like proteinase. CC2.
 XX The proteinases can be used in human or veterinary medicine and
 XX also be used as an immunostimulant or in the preparation of an
 XX immunostimulant to treat immunodeficiencies arising from (a) g
 XX lymphoid, myeloma), trauma (e.g. burns, wounds, surgery), medical
 XX treatment (e.g. with drugs such as steroids, cyclosporin and)
 XX genetic abnormalities (e.g. in combined immunodeficiency patients
 XX lacking B or T cells), diseases and old age. The proteinases can
 XX also be used in the treatment or prevention of diseases or
 XX conditions which respond to increased nitric oxide (NO) production,
 XX or as an antimicrobial agent or the component of an antimicrobial
 XX agent.
 XX
 S0 Sequence 186 AA;
 Query Match 88.0%; Score 95; DB 21; Length 186;
 Best Local Similarity 89.5%; Pied No. 2,79-08;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 POSTIMEDVAVTSYXKON 20
 Db 1 POSTIMEDVAVTSYXKON 19
 RESULT 9
 ID AAV8101 standard; Protein 186 AA.
 XX
 MC AAV8101;
 XX
 XX 04-JUL-2000 (first entry)
 XX
 DB 571 proteinases from pineapple stem.
 XX
 XX Proteinase; pineapple; treatment; prevention; prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX human immunodeficiency virus; malaria; malnutrition; trauma; burn;
 XX surgery; genetic abnormality; diabetes; nitric oxide; NO;
 XX anticarcinogenic.
 XX
 OS Ananas comosus.
 XX
 XX Key location/Qualifiers
 XX
 XX MISC-difference 20
 XX /note= 'Unidentified amino acids'
 XX
 XX MO200014253-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 24-AUG-1999; 99MC-G802784.
 XX
 XX 02-SEP-1998; 99GB-0019138.
 XX
 XX 02-SEP-1998; 99GB-0019138.

XX
 PA (CORT-) CORTECS UK LTD.
 XX
 PA Myocot TL, Crosseatt B;
 XX
 DB WP1: 2000-265998/22.
 XX
 DB N-PSDB: AA293185.
 XX
 PR Stem bromelain-like proteinases useful for the prevention and treatment
 PR of cancer and diseases of condition which respond to increased nitric
 PR oxide production are encoded by nucleic acid sequences isolated from a
 PR pineapple stem -
 XX
 XX
 XX Claim 4: Page 50-51: 72pp: English.
 XX
 XX The sequences encoding proteinases from pineapple stem have
 XX the same activity as a stem bromelain-like proteinase. CC2.
 XX The proteinases can be used in human or veterinary medicine and
 XX also be used as an immunostimulant or in the preparation of an
 XX immunostimulant to treat immunodeficiencies arising from (a) g
 XX lymphoid, myeloma), trauma (e.g. burns, wounds, surgery), medical
 XX treatment (e.g. with drugs such as steroids, cyclosporin and)
 XX genetic abnormalities (e.g. in combined immunodeficiency patients
 XX lacking B or T cells), diseases and old age. The proteinases can
 XX also be used in the treatment or prevention of diseases or
 XX conditions which respond to increased nitric oxide (NO) production,
 XX or as an antimicrobial agent or the component of an antimicrobial
 XX agent.
 XX
 S0 Sequence 186 AA;
 Query Match 88.0%; Score 95; DB 21; Length 186;
 Best Local Similarity 89.5%; Pied No. 2,79-08;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 POSTIMEDVAVTSYXKON 20
 Db 1 POSTIMEDVAVTSYXKON 19
 RESULT 10
 ID AAV8109 standard; Protein 187 AA.
 XX
 MC AAV8109;
 XX
 XX 04-JUL-2000 (first entry)
 XX
 DB 571 proteinases from pineapple stem.
 XX
 XX Proteinase; pineapple; treatment; prevention; prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX human immunodeficiency virus; malaria; malnutrition; trauma; burn;
 XX surgery; genetic abnormality; diabetes; nitric oxide; NO;
 XX anticarcinogenic.
 XX
 OS Ananas comosus.
 XX
 XX Key location/Qualifiers
 XX
 XX MISC-difference 20
 XX /note= 'Unidentified amino acids'
 XX
 XX MO200014253-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 24-AUG-1999; 99MC-G802784.
 XX
 XX 02-SEP-1998; 99GB-0019138.
 XX
 XX (CORT-) CORTECS UK LTD.

DR WPI; 2000-256998/22.

XX
XX
XX

PT Stem bromelain-like proteinases useful for the prevention and treatment of cancer and diseases which are caused by cancer.

XX pineapple stem -
PT oxalic acid production are encoded by nucleic acid sequences isolated from
the plant.
FI or cancer and diseases of colonists which respond to increased levels of
oxalate.
BT Claim 4; Page 61; 72pp; English.

AA The sequences encoding proteinases from pineapple stem have

the same activity as a stem bromelain-like proteinase, CCX2

CC can be used for treating or preventing cancer, e.g. solid tumours;
CC and proteases can be used in human or veterinary medicine and

non-solid tumours and virus induced tumours. The proteinases can

also be used as an immunostimulant or in the preparation of an immunostimulant to treat immunodeficiencies arising from

CC malnutrition, infection (e.g. HIV and malaria), tumours (e.g. breast and prostate cancer).

CC treatment (e.g. with drugs such as steroids, cyclosporin and

CC cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
CC creatine phosphate (CP) (inhibited in various conditions)

CC lacking B or T cells), diabetes and old age. The proteinase can

CC also be used in the treatment or prevention of diseases or conditions which respond to increased nitric oxide (NO) production

or as an antimicrobial agent or the component of an antimicrobial

CC agent.
XX

SQ Sequence 190 AA;

Query Match RA: 00 Score 95 DB 21 Length 190:

Best Local Similarity 89.5%; Pred. No. 2.8e-08;

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0
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QY 2 POSIDWRDYGAVTSVRNON 20

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OM protein - protein search, using sw model

Run on: November 21, 2002, 15:59:31 Search time 31 seconds

(without alignments) 65,968 Million cell updates/sec

Title: US-09-674-738-2

Sequence: 1 VP031PMNDQAVSVNQD 20

Scoring table: BLDSNM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 13250627 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0

Maximum Match 100

Listing filter 0: summarize

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22:	/S1022/Gcgdata/geneeq/geneeq-emb1/AA2002.DAT*

Page No. 4: the number of results predicted by class 4
score greater than 0.0 equals to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

No.	Score	Query	Length	DB ID	Description
1	105	100.0	20	11	AA0801
2	105	100.0	20	13	AA0801
3	105	100.0	20	21	AA0801
4	105	100.0	35	21	AA0801
5	100	95.2	21	21	AA0801
6	100	95.2	21	21	AA0801
7	93	88.6	20	21	AA0801
8	93	88.6	21	15	AA0801
9	88	83.6	21	21	AA0801

11	85	81.0	21	21	AA0801	N-terminal peptide
12	80	31.1	21	21	AA0801	710 proteins from
13	80	31.1	21	21	AA0801	524 proteins from
14	80	31.1	21	21	AA0801	Cytosolic protein
15	80	31.1	21	21	AA0801	Cytosolic protein
16	80	31.1	21	21	AA0801	Cytosolic protein
17	80	31.1	21	21	AA0801	Cytosolic protein
18	80	31.1	21	21	AA0801	Cytosolic protein
19	80	31.1	21	21	AA0801	Cytosolic protein
20	80	31.1	21	21	AA0801	Cytosolic protein
21	80	31.1	21	21	AA0801	Cytosolic protein
22	80	31.1	21	21	AA0801	Cytosolic protein
23	80	31.1	21	21	AA0801	Cytosolic protein
24	80	31.1	21	21	AA0801	Cytosolic protein
25	80	31.1	21	21	AA0801	Cytosolic protein
26	80	31.1	21	21	AA0801	Cytosolic protein
27	80	31.1	21	21	AA0801	Cytosolic protein
28	80	31.1	21	21	AA0801	Cytosolic protein
29	80	31.1	21	21	AA0801	Cytosolic protein
30	80	31.1	21	21	AA0801	Cytosolic protein
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32	80	31.1	21	21	AA0801	Cytosolic protein
33	80	31.1	21	21	AA0801	Cytosolic protein
34	80	31.1	21	21	AA0801	Cytosolic protein
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36	80	31.1	21	21	AA0801	Cytosolic protein
37	80	31.1	21	21	AA0801	Cytosolic protein
38	80	31.1	21	21	AA0801	Cytosolic protein
39	80	31.1	21	21	AA0801	Cytosolic protein
40	80	31.1	21	21	AA0801	Cytosolic protein
41	80	31.1	21	21	AA0801	Cytosolic protein
42	80	31.1	21	21	AA0801	Cytosolic protein
43	80	31.1	21	21	AA0801	Cytosolic protein
44	80	31.1	21	21	AA0801	Cytosolic protein
45	80	31.1	21	21	AA0801	Cytosolic protein

ALIGNMENTS

1	AA0801	standard; peptide; 20 AA.
2	AA0801	standard; peptide; 20 AA.
3	AA0801	standard; peptide; 20 AA.
4	AA0801	standard; peptide; 20 AA.
5	AA0801	standard; peptide; 20 AA.
6	AA0801	standard; peptide; 20 AA.
7	AA0801	standard; peptide; 20 AA.
8	AA0801	standard; peptide; 20 AA.
9	AA0801	standard; peptide; 20 AA.
10	AA0801	standard; peptide; 20 AA.
11	AA0801	standard; peptide; 20 AA.
12	AA0801	standard; peptide; 20 AA.
13	AA0801	standard; peptide; 20 AA.
14	AA0801	standard; peptide; 20 AA.
15	AA0801	standard; peptide; 20 AA.
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31	AA0801	standard; peptide; 20 AA.
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33	AA0801	standard; peptide; 20 AA.
34	AA0801	standard; peptide; 20 AA.
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36	AA0801	standard; peptide; 20 AA.
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40	AA0801	standard; peptide; 20 AA.
41	AA0801	standard; peptide; 20 AA.
42	AA0801	standard; peptide; 20 AA.
43	AA0801	standard; peptide; 20 AA.
44	AA0801	standard; peptide; 20 AA.
45	AA0801	standard; peptide; 20 AA.

CC cancer, parasites or pathogen infections. They can be used as an
 CC immunopressant, autolysis, cancer, parasite, pathogen infection,
 CC or transplant rejection by a host, allergic reactions, toxic shock or
 CC apoptosis. The fractions and proteins may also be used to prepare agents
 CC for the treatment of the above diseases and conditions.

80 Sequence 28 AA:

Query Match 100.0% Score 105, DB 21, Length 28:

Best Local Similarity 100.0% Pred. No. 2,3e-10:

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VPQSDHDSQAVTSVKNQ 20

DB 1 VPQSDHDSQAVTSVKNQ 20

RESULTS

ID AY84391 standard; peptide, 35 AA.

AY84391:

12-JUL-2000 (first entry)

N-terminal peptide from a fraction of bromelain designated C6/P2.

Bromelain, C6/P2, BRK-2 phosphorylation, intercalated, 24 kDa

growth factor, cytokine; cancer; parasite; pathogen infection;

immunopressant; autolysis, cancer, parasite, pathogen infection;

transplant rejection; allergic reaction; toxic shock; apoptosis.

XX Ananas comosus.

XX Key Location/Qualifiers

XX Misc-difference 25 /note= "not specified"

XX Misc-difference 20 /note= "not specified"

XX Misc-difference 30 /note= "not specified"

XX Misc-difference 33 /note= "not specified"

XX Misc-difference /note= "not specified"

XX WO200014254-A2.

XX 16-MAR-2000.

XX 24-AUG-1999; 99NO-GB02792.

XX 02-SEP-1998; 98GB-0019137.

XX (CORR.) CORTECS UK LTD.

XX Mycot TL, Peak K, Tyreman DR;

XX WPI: 2000-256999/22.

XX Bromelain fractions useful in the prevention and treatment of cancer,

XX parasites and pathogen infections and autoimmune diseases comprise

XX proteins with biological activity.

XX Claim 1, Page 51; 6pp; English.

XX The present sequence represents a N-terminal sequence from a fraction

XX of bromelain designated C6/P2, comprising proteins of molecular weights

XX 23.9 kDa and 26.6 kDa when measured by SDS-PAGE or 23.459 kDa and 23.6376

XX (leucine/tyrosine kinase) phosphorylation and MAP kinase cascade. They

XX also block interleukin-2 (IL-2) production and CD4+ T cell proliferation.

CC The bromelain fractions and proteins are used in medicine as they inhibit
 CC cancer, parasites or pathogen infections. They can be used as an
 CC immunopressant, autolysis, cancer, parasite, pathogen infection,
 CC or transplant rejection by a host, allergic reactions, toxic shock or
 CC apoptosis. The fractions and proteins may also be used to prepare agents
 CC for the treatment of the above diseases and conditions.

80 Sequence 35 AA:

Query Match 100.0% Score 105, DB 21, Length 35:

Best Local Similarity 100.0% Pred. No. 1e-10:

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VPQSDHDSQAVTSVKNQ 20

DB 1 VPQSDHDSQAVTSVKNQ 20

RESULTS

ID AY84394 standard; peptide, 21 AA.

AY84394:

12-JUL-2000 (first entry)

N-terminal peptide from a 24 kDa protein of bromelain.

Bromelain, C6/P2, BRK-2 phosphorylation, intercalated, 24 kDa

growth factor, cytokine; cancer; parasite; pathogen infection;

immunopressant; autolysis, cancer, parasite, pathogen infection;

transplant rejection; allergic reaction; toxic shock; apoptosis.

XX Ananas comosus.

XX Key Location/Qualifiers

XX Misc-difference 16 /note= "not specified"

XX WO200014254-A2.

XX 16-MAR-2000.

XX 24-AUG-1999; 99NO-GB02792.

XX 02-SEP-1998; 98GB-0019137.

XX (CORR.) CORTECS UK LTD.

XX Mycot TL, Peak K, Tyreman DR;

XX WPI: 2000-256999/22.

XX Bromelain fractions useful in the prevention and treatment of cancer,

XX parasites and pathogen infections and autoimmune diseases comprise

XX proteins with biological activity.

XX Claim 3, Page 52; 6pp; English.

XX The present sequence represents a N-terminal sequence from a 24 kDa

XX of bromelain designated C6/P2, comprising proteins of molecular weights

XX 23.9 kDa and 26.6 kDa when measured by SDS-PAGE or 23.459 kDa and 23.6376

XX (leucine/tyrosine kinase) phosphorylation and MAP kinase cascade. They

XX also block interleukin-2 (IL-2) production and CD4+ T cell proliferation.

XX The bromelain fractions and proteins are used in medicine as they inhibit

XX cancer, parasites or pathogen infections. They can be used as an

CC immunosuppressant for treating or preventing autoimmune diseases, graft or transplant rejection by a host; allergic reactions, toxic shock or apoptosis. The fractions and proteins may also be used to prepare agents for the treatment of the above diseases and conditions.

XX Sequence 21 AA;

Query Match 95.2%; Score 100; DB 21; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.1e-09; Mismatches 1; Indels 0; Gaps 0;
XX Matches 19; Conservative 0;
OY 1 VPQSLDMDGAGVTSVQNG 20
DB 1 VPQSLDMDGAGVTSVQNG 20

RESULT 5

ID AAH6802 standard; peptide, 20 AA.

XX AAH6802;

XX 24-NOV-1998 (first entry)

XX Comosain N-terminal sequence.

XX Comosain; bromelain; CCS; autoimmune; immunosuppressant;

XX graft rejection; anti-allergic; antiapoptosis; toxic shock;

XX antiparasitic; antipathogenic; anticancer; antitumor.

XX Annas comosus.

XX WQ9838291-A1.

XX 03-SEP-1998.

XX 25-FEB-1998; 98NC-0000590.

XX 25-MAR-1997; 97GB-0006119.

XX 25-FEB-1997; 97GB-0001327.

XX 25-FEB-1997; 97GB-0003850.

XX 28-FEB-1997; 97GB-0004252.

XX (CORT-1) CORTECS UK LTD.

XX Engwerda C, Wymott LJ, Peck K;

XX WPI; 1999-481194/1.

XX New isolated component of bromelain - used for treating e.g.

XX autoimmune diseases, transplant rejection, allergic reactions,

XX toxic shock, apoptosis, parasite or pathogen infections or cancer

XX Disclosure; Page 24; 56pp; English.

XX The patent discloses a fraction of bromelain, designated CCS, which

XX (1) contains proteins having molecular weights of 15,07 kD, 15.85 kD

XX and 27.45 kD (as determined by SDS-PAGE), (ii) has isoelectric points

XX in the range of 4.5 to 5.5, (iii) has a pI of 4.5 to 5.5, (iv) is soluble

XX in acetate buffer at pH 5.0; (b) separating the components by fast flow

XX high performance chromatography on S-Sepharose (RPM), eluting with a

XX collecting the fraction corresponding to the final double peak off the

XX column; and (d) isolating the protein from the fraction collected in (c).

XX pathways which control cell growth and proliferation; (b) for inhibiting

XX the production of growth factors and cytokines by cells; (c) for reducing

XX the production of growth factors and cytokines by cells; (d) for blocking

XX (e) as an immunosuppressive agent; (f) for blocking the production of

XX prevention of autoimmune diseases; graft or transplant rejection;

XX allergic reactions, toxic shock, apoptosis, parasite or pathogen

XX

CC infections, or cancer. The CCS fraction is postulated to consist of

CC the cysteine proteases annain and comosain, together with various other

XX components. The present sequence represents the N-terminal of comosain.

XX Sequence 20 AA;

Query Match 88.5%; Score 94; DB 10; Length 20.

XX Best Local Similarity 90.0%; Pred. No. 1.1e-08; Mismatches 1; Indels 0; Gaps 0;

OY 1 VPQSLDMDGAGVTSVQNG 20

DB 1 VPQSLDMDGAGVTSVQNG 20

RESULT 7

ID AAY51581 standard; peptide, 20 AA.

XX AAY51581;

XX 18-MAY-2000 (first entry)

XX Pineapple bromelain protease peptide fragment from fraction 4.

XX Bromelain; pineapple; protease; blood coagulation; inhibitor; plasmin.

XX Annas comosus.

XX WQ200003729-A1.

XX 27-JAN-2000.

XX 15-JUL-1998; 98NC-EP04406.

XX 15-JUL-1998; 98NC-EP04406.

XX (URSA-1) USAPAHK AR2NEIMITTEL OMH

XX Maurer R, Bockert K, Grabowska E, Eschmann K;

XX WPI; 2000-182338/16.

XX Composition for inhibiting blood coagulation more efficiently than

XX crude bromelain powder comprises bromelain proteases -

XX Claim 6; Page 15; 24pp; German.

XX This invention describes a novel use of bromelain proteases (I) for

XX inhibiting blood coagulation. (i) stimulate formation of plasmin, but

XX inhibit both formation of fibrin and adhesion of thrombocytes to

XX collagen. (ii) stimulate formation of plasminogen activator (t-PA) in

XX crude powder, e.g. comparable with streptokinase. AAY51581 and AAY51582

XX represent bromelain proteases isolated from pineapple (Ananas comosus)

XX which are used in the method of the invention.

XX Sequence 20 AA;

Query Match 88.5%; Score 93; DB 21; Length 20.

XX Best Local Similarity 94.1%; Pred. No. 1.6e-08; Mismatches 1; Indels 0; Gaps 0;

OY 1 VPQSLDMDGAGVTSVQNG 19

DB 1 VPQSLDMDGAGVTSVQNG 19

RESULT 8

ID AA47550 standard; protein, 213 AA.

XX AA47550;

PT 18-JUL-1994 (first entry)
 XX Stem bromelain protease.
 XX Proteolytic enzyme; cysteine protease; diarrhoea, fluid secretion;
 XX gastro-intestinal tract; GI tract; absorption.
 XX
 XX Ananas comosus.
 XX
 XX W09400147-A.
 XX
 XX 06-JAN-1994.
 XX
 XX 30-JUN-1993; 93NO-G801374.
 XX
 XX 30-JUN-1993; 93DB-0001866.
 XX 20-APR-1993; 93DB-0001866.
 XX 25-JUN-1993; 93DB-0001869.
 XX (CONT-) CORTECS LTD.
 XX
 XX Mycotec TL.
 XX
 XX WPI: 1994-025889/33.
 XX Enzyme, esp. bromelain contg. compn. for control of diarrhoea -
 PT esp. when caused by heat-labile toxin-producing E. coli; also
 XX inhibits fluid secretion in the gut and promotes absorption
 XX
 XX Disclosure: Page 11-13; 70pp; English.
 XX
 XX The sequence is that of stem bromelain protease, a mixture of
 CC various moieties derived from the stem of the pineapple. The
 CC protein is a cysteine protease used to treat infectious diarrhoea
 CC caused by heat-labile toxin-producing E. coli.
 CC and Vibrio cholerae. The enzyme reduces toxin binding activity,
 CC inhibits the secretory effect of the toxins and prevents attachment
 CC caused by enterococci, e.g. P827, thymophyllins, etc., and has no
 CC adverse effect on nucleic acid intlux.
 XX
 XX Sequence 213 AA:
 XX
 XX Query Match 88.4% Score 93; DB 15; Length 213;
 XX Local Similarity 94.7%; Pred. No. 2,467; Indels 0; Gaps 0;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX 2 VP0SIDMWDVATSYVNO 20
 XX
 XX 1 VP0SIDMWDVATSYVNO 19
 XX
 XX AAN68974 standard; protein: 213 AA.
 XX
 XX AAN68974;
 XX
 XX 09-AUG-1995 (first entry)
 XX
 XX Pineapple stem bromelain protease.
 XX
 XX Bromelain; protease; proteolytic enzyme; cholera, diphtheria; cancer;
 XX inflammation.
 XX
 XX Ananas comosus.
 XX
 XX W09500169-A.
 XX
 XX 05-JAN-1995.
 XX
 XX 24-JUN-1994; 94NO-C801168.
 XX

XX 25-JUN-1993; 93DB-0001188.
 XX (CONT-) CORTECS LTD.
 XX
 XX Mycotec TL.
 XX
 XX WPI: 1995-021751/07.
 XX Use of purified stem bromelain protease - to treat conditions
 XX dependent on cyclic nucleotide pathways e.g. cholera, diphtheria
 XX or cancer.
 XX
 XX Claim 1; Page 35; 45pp; English.
 XX
 XX Pineapple stem bromelain protease is used in the treatment of
 CC prophylaxis of conditions which are dependent on cyclic nucleotide
 CC and other intracellular and/or extracellular pathways. The disease
 CC infections such as cholera, diphtheria and pertussis.
 XX
 XX Sequence 213 AA:
 XX
 XX Query Match 88.4% Score 93; DB 16; Length 213;
 XX Local Similarity 94.7%; Pred. No. 2,467; Indels 0; Gaps 0;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX 1 VP0SIDMWDVATSYVNO 19
 XX 2 VP0SIDMWDVATSYVNO 20
 XX
 XX AAN64395 standard; peptide: 21 AA.
 XX
 XX AAN64395;
 XX
 XX 12-JUL-2000 (first entry)
 XX
 XX N-terminal peptide from a 26 kDa protein of bromelain.
 XX
 XX Bromelain; CC/P2; BHK-2 phosphorylation; interleukin-2;
 XX CD4+ T cell proliferation; mitogen activated protein kinase;
 XX growth factor; cytokines; cancer; parasites; protein kinases;
 XX immunomodulation; immunosuppression; immunoregulation;
 XX transplant rejection; allergic reaction; toxic shock; apoptosis.
 XX
 XX Ananas comosus.
 XX
 XX W0200014254-A2.
 XX
 XX 16-MAR-2000.
 XX
 XX 24-AUG-1999; 99NO-C802792.
 XX
 XX 02-SEP-1998; 98DB-0019137.
 XX (CONT-) CORTECS UK LTD.
 XX
 XX Mycotec TL, Peak K, Tyrean DR.
 XX
 XX WPI: 2000-26599/22.
 XX
 XX Bromelain fractions useful in the prevention and treatment of cancer,
 XX and in the treatment of cancer and autoimmune diseases comprise
 XX proteins with biological activity.
 XX

PS Claim 5: Page 52: 699: English.

The present sequence represents N-terminal sequence from a 24 kDa protein (as measured by SDS-PAGE). The protein is derived from a fraction containing 3.9 kDa and 26 kDa when measured by SDS-PAGE and 23.5 and 35.9 kDa and 36 kDa when measured by SDS-PAGE and 23.5 and 35.9 kDa when measured by mass spectrometry. The fraction blocks ERK-1 and ERK-2, also blocks interleukin-1 β production and COX-2 proliferation. The bromelain fractions and proteins are used in medicine as they inhibit cancer, parasites and cytokines. They can be used for treating cancer, parasites or pathogen infections. They can be used as an graft or transplant reaction by a host, allergic reactions, toxic shock or apoptosis. The fractions and proteins may also be used to treat cancer.

```

XX  Sequence 21 AA:
XX
XX  Query Match      63.8%; Score 88; DA 21; Length 21;
XX  Best Local Similarity 89.5%; Pred. Loc. 4.1e-07;
XX  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  1 VPSIDRSGKSVTSVNG 19
XX  ||||| ||||| |||||
XX  1 VPSIDRSGKSVTSVNG 19
XX
XX  1 VPSIDRSGKSVTSVNG 19
XX  ||||| ||||| |||||
XX  1 VPSIDRSGKSVTSVNG 19
XX

```

RESULT 11	
AA184396	
XX	AA184396 standard, peptide; 21 AA.
XX	
XX	AA184396;
XX	
XX	
XX	12-JUN-2000 (first entry)
XX	
XX	
XX	N-terminal peptide from a 24 kDa protein of bromelain.
XX	
XX	Bromelain; C5C/P2; 58K-2 phosphorylation; interleukin-2;
XX	B cell proliferation; mitogen activated protein kinase; MAP
XX	kinase; growth factor; cytokine; cancer; parasite; pathogen infection;
XX	transplant rejection; allergic reaction; toxic shock; apoptosis.

The present sequence represents a terminal sequence from a 24 kDa protein (as measured by SDS-PAGE). The protein is derived from a fraction containing 2.9 kDa and 3.6 kDa when measured by SDS-PAGE or 23 and 26 kDa when measured by mass spectrometry. The fraction blocks 88-92, also block interleukin-2 (IL-2) production and CD4⁺ T cell proliferation. The bromelain fractions and proteins are used in medicine as they inhibit cancer, parasite and pathogen infections. They can be used for treating produce growth factors and cytokines. They can be used for treating cancer, parasite or pathogen infections. They can be used as an adjuvant or transplant reaction by a host. Allergic reactions, toxic shock or sepsis. The present fractions and proteins may also be used to prepare agents

```

XX Sequence 21 AA;
QY Query Match 81.0%; Score 85; DB 21; Length 21;
   Best Local Similarity 85.0%; Pred. No. 3.5e-07;
   Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 1 VFSDIWRGSAVTSYKNG 20
   |||||
DB 1 VFSDIWRGSAVTSYKNG 20

```

RESULT 12
AAV83105
XX AAV83105 standard; Protein, 311 kDa.
XX
XX
XX AAV83105,
AC
XX
XX 04-JUL-2000 (first entry)
XX
XX 710 proteinase from pineapple stem.
DE

XX Proteolase; pinapple; treatment; virus induced tumour;
XX solid tumour; non-solid tumour; virus induced tumour;
XX immunostimulant; immunodeficiency; HIV;
XX human immunodeficiency virus; malaria; malnutrition; trauma; burn;
XX surgery; genetic abnormality; diabetes; nitric oxide; NO;
XX antitubercal..
XX
XX Anasas conicus.

XX	16-MAR-2000.	
XX	24-AUG-1999;	99HC-CB0784.
XX	02-SEP-1998;	98CF-C019138.
XX	(CORT-) CORTECS UK LTD.	

PL Mycott TL, Crosssett B.
 XX
 XX NFI: 2000-256938/22.
 XX N-PSDB: AZ93389.
 XX
 XX Stem bromelain-like proteinases useful for the prevention and treatment
 XX of cancer and diseases or conditions which respond to increased nitric
 XX oxide production are encoded by nucleic acid sequences isolated from a
 XX pineapple stem -

Claim 4; Page 58-59; 72pp; English.

CC also be used as an immunostimulant or in the preparation of an
 CC immunostimulant to treat immunodeficiencies arising from an
 CC malnutrition, infection (e.g. HIV and malaria), tumours (e.g.
 CC lymphoid, myeloma), trauma (e.g. burns, wounds, surgery), medical
 CC treatment (e.g. with drugs such as steroids, cyclosporin and
 CC cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
 CC ageing (e.g. in children), diabetes and old age. The protease can
 CC also be used in the treatment or prevention of diseases or
 CC as an anticarcinoma agent or the component of an anticarcinoma
 CC agent.
 CC conditions which respond to increased nitric oxide (NO) production,
 CC such as an anticarcinoma agent or the component of an anticarcinoma
 CC agent.
 CC Sequence 311 Mb.
 XX 50
 XX Query Match 80.0%; Score 84; DB 21; Length 111;
 XX Identical similarity 84.2%; Pred. No. 1,2e-05;
 XX Mismatch 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX 1 VP05IDR0GVANVENVNO 19
 XX Db 96 VP05IDR0GVANVENVNO 114
 XX
 XX RESULT 13
 XX AA893107
 XX ID AA893107 standard; Protein: 324 AA.
 XX AC AA893107;
 XX 04-JUL-2000 (first entry)
 XX DB D358484
 XX Protease; pinapple; treatment; prevention; prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX immunostimulant; immunodeficiency; HIV; malnutrition; trauma; burn;
 XX surgery; genetic abnormality; diabetes; nitric oxide; NO;
 XX anticarcinoma.
 XX Amino acid sequence:
 XX MW M0200014253-AL.
 XX PD 16-MAR-2000.
 XX XX 24-AUG-1999; 99NO-GB02784.
 XX PF 02-SEP-1998; 98GB-0019138.
 XX (CORT) CORTCS UK LTD.
 XX Myrcell TL, Crossell B;
 XX NPI: 2000-25698/72.
 XX N-PSDB: AA093393.
 XX Stem bromelain-like proteinases useful for the prevention and treatment
 XX of cancer and diseases or conditions which respond to increased nitric
 XX oxide production are encoded by nucleic acid sequences isolated from a
 XX pineapple stem.
 XX PT
 XX Claim 4; Page 64-66; 72pp; English.
 XX The sequences encoding proteinases from pineapple stem have
 XX the same activity as a stem bromelain-like proteinase, CM2,
 XX can be used for treating or preventing cancer, e.g. solid tumours;
 XX non-solid tumours and virus induced tumours. The proteinases can
 XX also be used as an immunostimulant or in the preparation of an
 XX immunostimulant to treat immunodeficiencies arising from an
 XX malnutrition, infection (e.g. HIV and malaria), tumours (e.g.
 XX lymphoid, myeloma), trauma (e.g. burns, wounds, surgery), medical
 XX treatment (e.g. with drugs such as steroids, cyclosporin and
 XX cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
 XX ageing (e.g. in children), diabetes and old age. The protease can
 XX also be used in the treatment or prevention of diseases or
 XX as an anticarcinoma agent or the component of an anticarcinoma
 XX agent.

CC lymphoid, myeloma), trauma (e.g. burns, wounds, surgery), medical
 CC treatment (e.g. with drugs such as steroids, cyclosporin and
 CC cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
 CC ageing (e.g. in children), diabetes and old age. The protease can
 CC also be used in the treatment or prevention of diseases or
 CC as an anticarcinoma agent or the component of an anticarcinoma
 CC agent.
 CC conditions which respond to increased nitric oxide (NO) production,
 CC such as an anticarcinoma agent or the component of an anticarcinoma
 CC agent.
 CC Sequence 324 Mb.
 XX 50
 XX Query Match 80.0%; Score 84; DB 21; Length 334;
 XX Identical similarity 84.4%; Pred. No. 1,2e-05;
 XX Mismatch 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX 1 VP05IDR0GVANVENVNO 19
 XX Db 96 VP05IDR0GVANVENVNO 114
 XX
 XX RESULT 14
 XX AA893104
 XX ID AA893104 standard; Protein: 351 AA.
 XX AC AA893104;
 XX 04-JUL-2000 (first entry)
 XX DB 674
 XX Protease; pinapple; treatment; prevention; prophylaxis; tumour;
 XX solid tumour; non-solid tumour; virus induced tumour;
 XX immunostimulant; immunodeficiency; HIV; malnutrition; trauma; burn;
 XX surgery; genetic abnormality; diabetes; nitric oxide; NO;
 XX anticarcinoma.
 XX Amino acid sequence:
 XX MW M0200014253-AL.
 XX PD 16-MAR-2000.
 XX XX 24-AUG-1999; 99NO-GB02784.
 XX PF 02-SEP-1998; 98GB-0019138.
 XX (CORT) CORTCS UK LTD.
 XX Myrcell TL, Crossell B;
 XX NPI: 2000-25698/72.
 XX N-PSDB: AA093393.
 XX Stem bromelain-like proteinases useful for the prevention and treatment
 XX of cancer and diseases or conditions which respond to increased nitric
 XX oxide production are encoded by nucleic acid sequences isolated from a
 XX pineapple stem.
 XX PT
 XX Claim 4; Page 55-57; 72pp; English.
 XX The sequences encoding proteinases from pineapple stem have
 XX the same activity as a stem bromelain-like proteinase, CM2,
 XX can be used for treating or preventing cancer, e.g. solid tumours;
 XX non-solid tumours and virus induced tumours. The proteinases can
 XX also be used as an immunostimulant or in the preparation of an
 XX immunostimulant to treat immunodeficiencies arising from an
 XX malnutrition, infection (e.g. HIV and malaria), tumours (e.g.
 XX lymphoid, myeloma), trauma (e.g. burns, wounds, surgery), medical
 XX treatment (e.g. with drugs such as steroids, cyclosporin and
 XX cyclophosphamide), protein loss (e.g. in diarrhoea and burns),
 XX ageing (e.g. in children), diabetes and old age. The protease can
 XX also be used in the treatment or prevention of diseases or
 XX as an anticarcinoma agent or the component of an anticarcinoma
 XX agent.

CC genetic abnormalities (e.g. in combined immunodeficiency patients
 CC also be used in the treatment of prevention of diseases or
 CC conditions which respond to increased nitric oxide (NO) production,
 CC as an antimicrobial agent or the component of an antimicrobial
 agent.

XX Sequence 351 AA;

Query Match 80.0%; Score 84; DB 21; Length 351;

Best Local Similarity 84.2%; Pred. No. 1.3e-05;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VQSIDMRSGAVTSVQKQ 19

DB 123 VQSIDMRSGAVTSVQKQ 141

RESULT 15

AM89556

ID AM89556 standard; protein: 377 AA.

AC AM89556;

XX 16-MAR-1999 (first entry)

XX Triticum sp. cysteine proteinase #1.

DE Triticum sp. cysteine proteinase; gluten; baking.

OS Triticum sp.

PK JP10327886-A.

XX 15-DEC-1998.

PD 27-MAR-1998; 98JP-0098140.

XX 31-MAR-1997; 97JP-0145946.

PA (GHOS) SHOMA SANGYO CO.

XX WPI, 1998-109255/10.

DR N-PSDB; AA082456.

XX New DNA coding cysteine proteinase originating from wheat seed -

PT useful for improving gluten for use in the bakery process

XX Claim 1; Page 15-16; 29pp; Japanese.

XX The present sequence represents a cysteine proteinase isolated from

CC wheat seed (Triticum sp.). The cysteine proteinase is useful for

CC improving gluten for use in the bakery process.

XX Sequence 377 AA;

Query Match 79.0%; Score 83; DB 20; Length 377;

Best Local Similarity 70.0%; Pred. No. 2.1e-05;

Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VQSIDMRSGAVTSVQKQ 20

DB 138 VQSIDMRSGAVTSVQKQ 157

Search completed: November 21, 2002, 16:08:39

Job time : 31 secs

GenScript version 5.1.3
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OW protein - protein search, using sw model

Run on: November 21, 2002, 15:59:48 | Search time 7.5 seconds
(without alignment) 110,604 Million cell updates/sec

Title: US-09-674-738-2

Sequence: 1 VSQSIWSSGATSVNKG 20

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 112692 seqs, 417638 residues

Total number of hits satisfying chosen parameters: 112692

Mitman DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Mitman Match 0%

Maximum Match 100%

Clustering time 155 minutes

Database: SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SWIMMATES

Result No.	Score	Match	Length	ID	Description
1	88.6	212	1	BROW_NAKO	P14518 anas cano
2	88.6	212	1	PAF2_NAKO	P14518 anas cano
3	84.0	352	1	PAF2_NAKO	P14518 anas cano
4	82.7	352	1	PAF2_NAKO	P14518 anas cano
5	82.7	352	1	PAF2_NAKO	P14518 anas cano
6	82.7	352	1	PAF2_NAKO	P14518 anas cano
7	82.7	352	1	PAF2_NAKO	P14518 anas cano
8	82.7	352	1	PAF2_NAKO	P14518 anas cano
9	82.7	352	1	PAF2_NAKO	P14518 anas cano
10	82.7	352	1	PAF2_NAKO	P14518 anas cano
11	82.7	352	1	PAF2_NAKO	P14518 anas cano
12	82.7	352	1	PAF2_NAKO	P14518 anas cano
13	82.7	352	1	PAF2_NAKO	P14518 anas cano
14	82.7	352	1	PAF2_NAKO	P14518 anas cano
15	82.7	352	1	PAF2_NAKO	P14518 anas cano
16	82.7	352	1	PAF2_NAKO	P14518 anas cano
17	82.7	352	1	PAF2_NAKO	P14518 anas cano
18	82.7	352	1	PAF2_NAKO	P14518 anas cano
19	82.7	352	1	PAF2_NAKO	P14518 anas cano
20	82.7	352	1	PAF2_NAKO	P14518 anas cano
21	82.7	352	1	PAF2_NAKO	P14518 anas cano
22	82.7	352	1	PAF2_NAKO	P14518 anas cano
23	82.7	352	1	PAF2_NAKO	P14518 anas cano
24	82.7	352	1	PAF2_NAKO	P14518 anas cano
25	82.7	352	1	PAF2_NAKO	P14518 anas cano
26	82.7	352	1	PAF2_NAKO	P14518 anas cano
27	82.7	352	1	PAF2_NAKO	P14518 anas cano
28	82.7	352	1	PAF2_NAKO	P14518 anas cano
29	82.7	352	1	PAF2_NAKO	P14518 anas cano
30	82.7	352	1	PAF2_NAKO	P14518 anas cano
31	82.7	352	1	PAF2_NAKO	P14518 anas cano
32	82.7	352	1	PAF2_NAKO	P14518 anas cano
33	82.7	352	1	PAF2_NAKO	P14518 anas cano

34	68.6	333	1	CATL_HUMAN	P25734 hmoa sapien
35	68.6	333	1	TRSL_RAT	P15522 ratu mus
36	68.6	333	1	CATL_BOVIN	P25925 bos tauru
37	68.6	333	1	CATL_BOVIN	P25925 bos tauru
38	68.6	333	1	CATL_BOVIN	P25925 bos tauru
39	68.6	333	1	CATL_BOVIN	P25925 bos tauru
40	68.6	333	1	CATL_BOVIN	P25925 bos tauru
41	68.6	333	1	CATL_BOVIN	P25925 bos tauru
42	68.6	333	1	CATL_BOVIN	P25925 bos tauru
43	68.6	333	1	CATL_BOVIN	P25925 bos tauru
44	68.6	333	1	CATL_BOVIN	P25925 bos tauru
45	68.6	333	1	CATL_BOVIN	P25925 bos tauru
46	68.6	333	1	CATL_BOVIN	P25925 bos tauru
47	68.6	333	1	CATL_BOVIN	P25925 bos tauru
48	68.6	333	1	CATL_BOVIN	P25925 bos tauru
49	68.6	333	1	CATL_BOVIN	P25925 bos tauru
50	68.6	333	1	CATL_BOVIN	P25925 bos tauru
51	68.6	333	1	CATL_BOVIN	P25925 bos tauru
52	68.6	333	1	CATL_BOVIN	P25925 bos tauru
53	68.6	333	1	CATL_BOVIN	P25925 bos tauru
54	68.6	333	1	CATL_BOVIN	P25925 bos tauru
55	68.6	333	1	CATL_BOVIN	P25925 bos tauru
56	68.6	333	1	CATL_BOVIN	P25925 bos tauru
57	68.6	333	1	CATL_BOVIN	P25925 bos tauru
58	68.6	333	1	CATL_BOVIN	P25925 bos tauru
59	68.6	333	1	CATL_BOVIN	P25925 bos tauru
60	68.6	333	1	CATL_BOVIN	P25925 bos tauru
61	68.6	333	1	CATL_BOVIN	P25925 bos tauru
62	68.6	333	1	CATL_BOVIN	P25925 bos tauru
63	68.6	333	1	CATL_BOVIN	P25925 bos tauru
64	68.6	333	1	CATL_BOVIN	P25925 bos tauru
65	68.6	333	1	CATL_BOVIN	P25925 bos tauru
66	68.6	333	1	CATL_BOVIN	P25925 bos tauru
67	68.6	333	1	CATL_BOVIN	P25925 bos tauru
68	68.6	333	1	CATL_BOVIN	P25925 bos tauru
69	68.6	333	1	CATL_BOVIN	P25925 bos tauru
70	68.6	333	1	CATL_BOVIN	P25925 bos tauru
71	68.6	333	1	CATL_BOVIN	P25925 bos tauru
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74	68.6	333	1	CATL_BOVIN	P25925 bos tauru
75	68.6	333	1	CATL_BOVIN	P25925 bos tauru
76	68.6	333	1	CATL_BOVIN	P25925 bos tauru
77	68.6	333	1	CATL_BOVIN	P25925 bos tauru
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79	68.6	333	1	CATL_BOVIN	P25925 bos tauru
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82	68.6	333	1	CATL_BOVIN	P25925 bos tauru
83	68.6	333	1	CATL_BOVIN	P25925 bos tauru
84	68.6	333	1	CATL_BOVIN	P25925 bos tauru
85	68.6	333	1	CATL_BOVIN	P25925 bos tauru
86	68.6	333	1	CATL_BOVIN	P25925 bos tauru
87	68.6	333	1	CATL_BOVIN	P25925 bos tauru
88	68.6	333	1	CATL_BOVIN	P25925 bos tauru
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90	68.6	333	1	CATL_BOVIN	P25925 bos tauru
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92	68.6	333	1	CATL_BOVIN	P25925 bos tauru
93	68.6	333	1	CATL_BOVIN	P25925 bos tauru
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99	68.6	333	1	CATL_BOVIN	P25925 bos tauru
100	68.6	333	1	CATL_BOVIN	P25925 bos tauru

	Query Match	78.0%
	Best Local Similarity	76.00%
Matches:	14;	Conservative
	4;	Mismatches
	2;	Indels
	0;	Gaps

[illegible]

Mon Nov 25 08:17:59 2002

[illegible][illegible]

GenCore version 5.1.3
Copyright (c) 1999 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 11:59:48 / Search time 3.5 seconds

Title: US-09-674-738-1 110,604 Million call updates/sec

Sequence: 1 VSQSDIDRVDYANVSXKNN 20

Scoring table: BLOSUM62

Gapop 10.0, Gapex 0.5

Searched: 112892 seqs, 4147613 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 similarities

Databases: SwissProt_40%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the local score distribution.

SNOWKIDS

Result No.	Score	Match	Length	DB ID	Description
1	18.1	345	1	ANNU_ANNO	P40364 anas com
2	93	36.1	1	ANNU_ANNO	P40364 anas com
3	78	72.2	1	BD12_ADAP	P43496 carica ppa
4	75	60.4	1	CAV2_CAV2	P43496 carica ppa
5	75	60.4	1	CAV2_CAV2	P43496 carica ppa
6	74	68.5	1	CC3_CCN3	P32355 carica can
7	74	68.5	1	CC3_CCN3	P32355 carica can
8	74	68.5	1	CC3_CCN3	P32355 carica can
9	74	68.5	1	CC3_CCN3	P32355 carica can
10	74	68.5	1	CC3_CCN3	P32355 carica can
11	74	68.5	1	CC3_CCN3	P32355 carica can
12	74	68.5	1	CC3_CCN3	P32355 carica can
13	74	68.5	1	CC3_CCN3	P32355 carica can
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20	74	68.5	1	CC3_CCN3	P32355 carica can
21	74	68.5	1	CC3_CCN3	P32355 carica can
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31	74	68.5	1	CC3_CCN3	P32355 carica can
32	74	68.5	1	CC3_CCN3	P32355 carica can
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34	65	61.1	1	BD12_ADAP	P43496 carica ppa
35	65	60.2	1	CAV2_CAV2	P43496 carica ppa
36	65	60.2	1	CAV2_CAV2	P43496 carica ppa
37	65	60.2	1	CAV2_CAV2	P43496 carica ppa
38	65	60.2	1	CAV2_CAV2	P43496 carica ppa
39	64	59.3	1	CC3_CCN3	P32355 carica can
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41	64	59.3	1	CC3_CCN3	P32355 carica can
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44	64	59.3	1	CC3_CCN3	P32355 carica can
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46	63	58.3	1	CC3_CCN3	P32355 carica can
47	63	58.3	1	CC3_CCN3	P32355 carica can
48	63	58.3	1	CC3_CCN3	P32355 carica can
49	63	58.3	1	CC3_CCN3	P32355 carica can
50	63	58.3	1	CC3_CCN3	P32355 carica can

ALIGNMENTS

Result No.	Score	Match	Length	DB ID	Description
1	18.1	345	1	ANNU_ANNO	P40364 anas com
2	93	36.1	1	ANNU_ANNO	P40364 anas com
3	78	72.2	1	BD12_ADAP	P43496 carica ppa
4	75	60.4	1	CAV2_CAV2	P43496 carica ppa
5	75	60.4	1	CAV2_CAV2	P43496 carica ppa
6	74	68.5	1	CC3_CCN3	P32355 carica can
7	74	68.5	1	CC3_CCN3	P32355 carica can
8	74	68.5	1	CC3_CCN3	P32355 carica can
9	74	68.5	1	CC3_CCN3	P32355 carica can
10	74	68.5	1	CC3_CCN3	P32355 carica can
11	74	68.5	1	CC3_CCN3	P32355 carica can
12	74	68.5	1	CC3_CCN3	P32355 carica can
13	74	68.5	1	CC3_CCN3	P32355 carica can
14	74	68.5	1	CC3_CCN3	P32355 carica can
15	74	68.5	1	CC3_CCN3	P32355 carica can
16	74	68.5	1	CC3_CCN3	P32355 carica can
17	74	68.5	1	CC3_CCN3	P32355 carica can
18	74	68.5	1	CC3_CCN3	P32355 carica can
19	74	68.5	1	CC3_CCN3	P32355 carica can
20	74	68.5	1	CC3_CCN3	P32355 carica can
21	74	68.5	1	CC3_CCN3	P32355 carica can
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33	74	68.5	1	CC3_CCN3	P32355 carica can

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Query Match      100.0% Score 108. DB 1: Length 212;
Best Local Similarity 100.0% Pred. No. 2.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 1 VQSDIMEDYQVTSVNNQ 20
DB 2 VQSDIMEDYQVTSVNNQ 21

RESULT 2
ANAN ANACO
ID ANAN ANACO STANDARD; PRT: 345 AA.
DT 01-NOV-1987 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
AN Anakin precursor (EC 3.4.22.31)
GN ANAKIN
NC Eukaryotic Pileup(s).
CC Serpinthyrin, Magnoliophyta; Liliopsida; Comelinales; Incerates sedis;
CC Oxycaryon, Magnoliophyta; Liliopsida; Comelinales; Incerates sedis;
CC NCBI TaxId=4615.
RC ANAKIN FROM N.A.
RC STRAIN=CV Smooth Cayenne; TISSUE=stem;
RC Robertson C.E., Goodenough P.M.;
RC Identifying an anakin gene from pineapple." ;
RC Nucleic Acid Res. 1997; 25: 4893-4897.
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[illegible]

UT	15-JUN-1998 (Rel. 36, Created)
OT	15-JUN-1998 (Rel. 36, Last sequence update)
CT	Catechol O-methyltransferase (EC 2.1.1.7) [SNCLII]
GC	Catechepin L precursor (EC 3.4.22.15) [SNCLII]
GM	Glucoamylase (EC 3.2.1.3) [SNCLII]
GL	Glucoamylase precursor (Blood fluke)
GO	Glyoxal oxidase (EC 1.1.3.1) [SNCLII]
OC	Schistosoma, Metazoa; Platyhelminthes; Trematoda; Digenea, Strigidae;
CC	Schistosoma, Metazoa; Schistosomidae; Schistosoma
CC	1997 taxid=18;
CC	SEQUENCE FROM N.A.
AP	MEDLINE:J010043;PubMed:73817L
RA	Smith A.M., Dalton J.P., Clough K.A., Kilbane C.L., Harrop S.A.,
SA	Wale N., Birdseye J.,Nimmi express catehespin L proteinase activity.",
MO	Mol. Biochem. Parasitol. 67:11-15(1994)
CC	- FUNCTION: WATERS CRUCIAL FOR METABOLISM OF HOST HEMOGLOBIN
CC	compared to catehespin B, catehespin L exhibits higher activity
CC	towards protein substrates, but has little activity on Z-Aig-Arg-
CC	carboxy peptide substrate.
CC	- SUBCELLULAR LOCATION: Lysosomal.
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC	This SMILES-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC	Geneva. The copyright holder grants permission to make copies of this
CC	entry for non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by for commercial
CC	purposes without prior written permission is prohibited. Please contact us
CC	or send an email to licencedata@sbcb.ch or see http://www.isib-sib.ch/announce/
CC	NSP_000317; IPNO_485;1; --
DR	MEMOS: C01.018; Peptidase C1;
DR	InterPro: IPR000166; Serine protease;
DR	Plant_F00012; Peptidase C1; 1 residue.
DR	PRINTS: PR007056 PAPAIN; Papain; C1; 1
DR	PROSITE: PS00139; THIOL PROTEASE CYS; 1
DR	PROSITE: PS00639; THIOL PROTEASE HS; 1
KM	Hydrolyse: thiol protease; Glycoprotein; Lysosome; Xyogen; Signal.
FT	1 SIGNAL
FT	1 307 POTENTIAL PEPTIDE POTENTIAL).
FT	CHAIN 105 319 CATHEPSIN L.
FT	ACT_SITE 329 329 BY SIMILARITY.
FT	ACT_SITE 266 266 BY SIMILARITY.
FT	ACT_SITE 286 286 BY SIMILARITY.
FT	DISHFID 126 167 BY SIMILARITY.
FT	DISHFID 258 307 BY SIMILARITY.
FO	SEQUENCE 319 AA; 36136 MW; 5CF6E6A3F1913479 CRC64,
QC	Query Match 67.6%; Score 73; DB I; Length 319.
OC	Best Local Similarity 61.2%; Word No. 0.00016;
MA	Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0.
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DB	105 INFSFGKGVAVNQ 123
CAIT3 PASHE	RESULT 11
CA1D GRAS FASHF	10 GRAS FASHF
OTC	01-F8B-1996 (Rel. 33, Created)
OT	01-F8B-1996 (Rel. 33, Last sequence update)
OT	Pucative catehespin L (EC 3.4.22.15) Newly excyted juvenile protein

DB 8) (Fragment).
 CC Faelcia hepatica (Liver fluke).
 CC Echinostoma, Echinostoma; Fasciolidae; Fasciola.
 CC NCBI_TaxID=192;
 CC MEDLINE=9346693; PubMed=763932;
 RA Thakuric J., Ahman K., Nemen E.;
 RA Fasciola hepatica rapid identification of newly excysted juvenile
 RA proteins
 BL Biochem. Biophys. Res. Comm. 231:169-174(1997).
 CC - CATALYTIC ACTIVITY: PROTEINASE; cleaves close to that of papain. An
 CC compared to cathepsin B, cathepsin B exhibits higher activity
 CC towards protein substrates, but has little activity on Z-Ag-Arg-
 CC - SUBUNIT: DIMER OF AN HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
 CC BONDS (POTENTIAL).
 CC - DEVELOPMENTAL LOCATION: Intestine (potential).
 CC - DEVELOPMENTAL STAGE: EXPRESSED AT THE EARLY, KNOWN STAGE JUVENILE
 CC STAGE.
 CC - SIMILARITY: BELONGS TO PERLIPASE FAMILY CL.
 CC InterPro: IPR000169; SIMPRO: acitie.
 CC Pfam: PF00115; Replicase CL1; AS CYS; PARTIAL.
 CC PROSITE: P00039; THIOI. PROTEASE HIS; PARTIAL.
 CC PROSITE: P00040; THIOI. PROTEASE ASN; PARTIAL.
 CC NON-TER: 19;
 CC SEQUENCE 471 AA; 50905 MW; 08F3D01935E8ED C6064;
 Query Match 66.7%; Score 72; PB 1; Length 47;
 Best Local Similarity 63.7%; Pctid No. 8:0039;
 Matched 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 1 VPSIDMDQYGVATSYNM 18
 DB 2 VPSIDMDQYGVATSYNM 19
 CC RESULT 13
 CC C02 CANCER STANDARD; PRT; 471 AA.
 ID C02 CANCER
 AC P25777; (Ref. 22, Created)
 DT 01-OCT-1993 (Ref. 22, Last annotation update)
 DT 15-JUN-2002 (Ref. 41, Last annotation update)
 DB Oryzias beta chain precursor (EC 3.4.22.-)
 CC Bakayev A., Vitoldarova, Streptococcus, Embryophyta, Trechophyta;
 CC Spermatophyta, Magnoliopsida; Liliopsida; Poales; Poaceae;
 CC Eriocaulaceae; Oryzae; Oryza.
 CC NCBI_TaxID=9731;
 CC MEDLINE=9403693; PubMed=821692;
 RA Matsumoto H., Abu K., Emori Y., Koyama H., Arai S.;
 RA Molecular cloning and gene structure of the cDNA expression of multiple
 RA Oryzias beta chain precursor (EC 3.4.22.-)
 BL J. Biol. Chem. 266:16897-16902(1991).
 CC - TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
 CC - SIMILARITY: BELONGS TO PERLIPASE FAMILY CL.
 CC InterPro: IPR000169; SIMPRO: acitie.
 CC Pfam: PF00115; Replicase CL1; AS CYS; PARTIAL.
 CC PROSITE: P00039; THIOI. PROTEASE HIS; PARTIAL.
 CC PROSITE: P00040; THIOI. PROTEASE ASN; PARTIAL.
 CC NON-TER: 19;
 CC SEQUENCE 471 AA; 50905 MW; 08F3D01935E8ED C6064;

CC entities requires a license agreement (see <http://www.lsb.ch.com/unice/>
 or send an email to license@lsb.ch).
 CC EMU: D00407; BAI4403.1;
 CC PIR: J03399; XBRZC.
 CC MEDLINE=9403693; PubMed=821692;
 RA Matsumoto H., Abu K., Emori Y., Koyama H., Arai S.;
 RA Molecular cloning and gene structure of the cDNA expression of multiple
 RA Oryzias beta chain precursor (EC 3.4.22.-)
 BL J. Biol. Chem. 266:16897-16902(1991).
 CC - TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
 CC - SIMILARITY: BELONGS TO PERLIPASE FAMILY CL.
 CC InterPro: IPR000169; SIMPRO: acitie.
 CC Pfam: PF00115; Replicase CL1; AS CYS; PARTIAL.
 CC PROSITE: P00039; THIOI. PROTEASE HIS; PARTIAL.
 CC PROSITE: P00040; THIOI. PROTEASE ASN; PARTIAL.
 CC NON-TER: 19;
 CC SEQUENCE 471 AA; 50905 MW; 08F3D01935E8ED C6064;
 Query Match 66.7%; Score 72; PB 1; Length 47;
 Best Local Similarity 63.7%; Pctid No. 8:0039;
 Matched 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 1 VPSIDMDQYGVATSYNM 19
 DB 140 LPSVDNRKCAVPMKNO 158
 CC RESULT 13
 CC C02 CANCER STANDARD; PRT; 43 AA.
 ID C02 CANCER
 AC P25777; (Ref. 22, Created)
 DT 01-OCT-1993 (Ref. 22, Last annotation update)
 DT 15-JUN-2002 (Ref. 41, Last annotation update)
 DB Oryzias beta chain precursor (EC 3.4.22.-)
 CC Bakayev A., Vitoldarova, Streptococcus, Embryophyta, Trechophyta;
 CC Spermatophyta, Magnoliopsida; Liliopsida; Poales; Poaceae;
 CC Eriocaulaceae; Oryzae; Oryza.
 CC NCBI_TaxID=9731;
 CC MEDLINE=9403693; PubMed=821692;
 RA Matsumoto H., Abu K., Emori Y., Koyama H., Arai S.;
 RA Molecular cloning and gene structure of the cDNA expression of multiple
 RA Oryzias beta chain precursor (EC 3.4.22.-)
 BL J. Biol. Chem. 266:16897-16902(1991).
 CC - TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
 CC - SIMILARITY: BELONGS TO PERLIPASE FAMILY CL.
 CC InterPro: IPR000169; SIMPRO: acitie.
 CC Pfam: PF00115; Replicase CL1; AS CYS; PARTIAL.
 CC PROSITE: P00039; THIOI. PROTEASE HIS; PARTIAL.
 CC PROSITE: P00040; THIOI. PROTEASE ASN; PARTIAL.
 CC NON-TER: 19;
 CC SEQUENCE 471 AA; 50905 MW; 08F3D01935E8ED C6064;

KW Hydrolase: Thiol protease.
 FT BY SIMILARITY.
 FT 43
 FT 43
 SQ SEQUENCE 43 AA: 456 MW; 1777ACB748C5F34B Length; 43
 Query Match: 68 78; Score 71; DB 1; Length 43;
 Best Local Similarity 68.4%; Pred. No. 4,7e+05;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 POSIDMRGQVNTSVNKN 20
 DB 2 POSVDWRGQVNTVPVQ 20
 RESULT 14
 ID GR1_ZINOF STANDARD; PRT; 221 AA.
 AC P82473;
 AC 30-MAY-2000 (Rel. 39, Created; Sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cysteine proteinase gp-1 (EC 3.4.22.-).
 DE Cysteine proteinase gp-1 (EC 3.4.22.-).
 OS Saktetoy; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Zingiberaceae;
 CC Zingiber.
 RN [1]_TaxID:94128.
 RP SOURCE: GenBank.
 RC MEDLINE:20156257; PubMed:10691991;
 RA Choi K.H., Lauren R.A.;
 RT Amino-acid sequence and glycan structures of cysteine proteases with
 RT Amino-acid sequence and glycan structures of cysteine proteases with
 RL Eur. J. Biochem. 267:1516-1524(2000)
 CC -/- CATALYTIC ACTIVITY: Preferential cleavage with a proline residue
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR HSSP: P00785; ZACT.
 DR GlycoSuiteDB:G0002674; Peptidase C1.
 DR InterPro: IPR000169; SHprot. acsite.
 DR Pfam: PF001126; Peptidase C1 1.
 DR ProDom: P000158; Peptidase C1 1.
 DR PROSITE: P000139; THIOL-PROTEASE; ASN; FALSE NEG.
 DR PROSITE: P00649; THIOL-PROTEASE; ASN; FALSE NEG.
 DR PROSITE: P00640; THIOL-PROTEASE; ASN; 1.
 DR Hydrolase: Thiol protease; Glycoprotein.
 KW ACT SITE 127, 127 BY SIMILARITY.
 FT ACT SITE 127, 127 BY SIMILARITY.
 FT DISULFID 54 65 BY SIMILARITY.
 FT DISULFID 58 69 BY SIMILARITY.
 FT DISULFID 155 296 BY SIMILARITY.
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...)
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...)
 SQ SEQUENCE 221 AA: 23922 MW; 909A312B98432D42 CRC64;
 Query Match: 68 78; Score 71; DB 1; Length 221;
 Best Local Similarity 68.4%; Pred. No. 0.00126; 4; Indels 0; Gaps 0;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VPQSIDMRGQVNTSVNKN 19
 DB 3 LPQSIDMRGQVNTVPVQ 21
 RESULT 15
 ID GR1_ZINOF STANDARD; PRT; 221 AA.
 AC P82473;
 AC 30-MAY-2000 (Rel. 39, Created; Sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cysteine proteinase gp-1 (EC 3.4.22.-).
 DE Cysteine proteinase gp-1 (EC 3.4.22.-).
 OS Saktetoy; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Zingiberaceae;
 CC Zingiber.
 RN [1]_TaxID:94128.
 RP SOURCE: GenBank.
 RC MEDLINE:20156257; PubMed:10691991;
 RA Choi K.H., Lauren R.A.;
 RT Amino-acid sequence and glycan structures of cysteine proteases with
 RT Amino-acid sequence and glycan structures of cysteine proteases with
 RL Eur. J. Biochem. 267:1516-1524(2000)
 CC -/- CATALYTIC ACTIVITY: Preferential cleavage with a proline residue
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR HSSP: P00785; ZACT.
 DR GlycoSuiteDB:G0002674; Peptidase C1.
 DR InterPro: IPR000169; SHprot. acsite.
 DR Pfam: PF001126; Peptidase C1 1.
 DR ProDom: P000158; Peptidase C1 1.
 DR PROSITE: P000139; THIOL-PROTEASE; ASN; FALSE NEG.
 DR PROSITE: P00649; THIOL-PROTEASE; ASN; FALSE NEG.
 DR PROSITE: P00640; THIOL-PROTEASE; ASN; 1.
 DR Hydrolase: Thiol protease; Glycoprotein.
 KW ACT SITE 127, 127 BY SIMILARITY.
 FT ACT SITE 127, 127 BY SIMILARITY.
 FT DISULFID 54 65 BY SIMILARITY.
 FT DISULFID 58 69 BY SIMILARITY.
 FT DISULFID 155 296 BY SIMILARITY.
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...)
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...)
 SQ SEQUENCE 221 AA: 23922 MW; 909A312B98432D42 CRC64;
 Query Match: 68 78; Score 71; DB 1; Length 221;
 Best Local Similarity 68.4%; Pred. No. 0.00126; 4; Indels 0; Gaps 0;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VPQSIDMRGQVNTSVNKN 19
 DB 3 LPQSIDMRGQVNTVPVQ 21

DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cysteine proteinase gp-1 (EC 3.4.22.-).
 DE Cysteine proteinase gp-1 (EC 3.4.22.-).
 OS Zingiber officinale (Ginger) Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Zingiberaceae;
 CC Zingiber.
 RN [1]_TaxID:94128;
 RP SEQUENCE.
 RC TRUSUR-ROOT;
 RA Choi K.H., Lauren R.A.;
 RT Amino-acid sequence and glycan structures of cysteine proteases with
 RT Amino-acid sequence and glycan structures of cysteine proteases with
 RL Eur. J. Biochem. 267:1516-1524(2000)
 CC -/- CATALYTIC ACTIVITY: Preferential cleavage with a proline residue
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 CC -/- CAUTION: THE AUTHORS REGARD THE SEQUENCE AS TENTATIVE, AS THEY
 CC BELIEVE THAT IT MAY HAVE BEEN CONTAMINATED BY A HOMOLOGOUS
 DR HSSP: P00785; ZACT.
 DR InterPro: IPR000668; Peptidase C1.
 DR InterPro: IPR000169; SHprot. acsite.
 DR PRINTS: PR00705; BABAIN_C1 1.
 DR ProDom: P000158; Peptidase C1 1.
 DR PROSITE: P000139; THIOL-PROTEASE; ASN; FALSE NEG.
 DR PROSITE: P00649; THIOL-PROTEASE; ASN; 1.
 DR PROSITE: P00640; THIOL-PROTEASE; ASN; 1.
 DR Hydrolase: Thiol protease; Glycoprotein.
 KW ACT SITE 161 161 BY SIMILARITY.
 FT ACT SITE 161 161 BY SIMILARITY.
 FT DISULFID 24 65 BY SIMILARITY.
 FT DISULFID 55 206 BY SIMILARITY.
 FT DISULFID 152 152 BY SIMILARITY.
 FT CARBOHYD 95 95 N-LINKED (GLCNAC...)
 FT CARBOHYD 152 152 N-LINKED (GLCNAC...)
 SQ SEQUENCE 221 AA: 24241 MW; 3035D7970EA74DB CRC64;
 Query Match: 65 78; Score 71; DB 1; Length 221;
 Best Local Similarity 68.4%; Pred. No. 0.00126;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VPQSIDMRGQVNTSVNKN 19
 DB 3 LPQSIDMRGQVNTVPVQ 21

Search completed: November 21, 2002. 16:09:01
 Job time : 8.5 secs

Rec'd Local Similarity (M. 24) Pr'd. No. 6.5e-06; Matches 46; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 POSIMRUSGANTVKNQ 20
DB 1 POSIMRANGATVKNQ 19

RESULT 9
QY98M8 PRELIMINARY; PRT, 277 AA.
AC Q98M8
DT 01-MAR-2000 (ITEMBELrel. 13; Created)
DT 01-MAR-2002 (ITEMBELrel. 20; Last annotation update)
DT 01-MAR-2002 (ITEMBELrel. 20; Last annotation update)
DB Chymopain isoform V (EC 3.4.22.6) (Fragment)
OS Carica papaya (papaya)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosales;
OC Nymphaeales; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae;
OC NCBT_TaxID=3649;
RN NCBT_TaxID=3649;
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF.

BA Taylor M.A., Al-Sheikh M., Revell D.F., Sumner I.O., Connerton I.F.,
ET in Escherichia coli expression of Carica papaya chymopain isoforms
RU Plant Sci. 145:41-47(1999).
RU Plant Sci. 145:41-47(1999).
UR RSP: P14680; IVAL
UR MEROPS; C01.002; ..; Peptidase Cl.
DR Pfam: Pf0112; Peptidase Cl.
DR InterPro: IP000169; SHPoc_aseite.
DR Pfam: Pf0112; Peptidase Cl.
UR ProDom: PD000158; Peptidase Cl.
UR ProDom: PD000158; Peptidase Cl.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
RW Hydrolase; Thiol protease.
SQ SEQUENCE 237 AA; 24721 MW; LCCVCSDTAFVAAH80 CDS64;

Query Match Similarity 80.0%; Score 84; DB 10; Length 227;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 POSIMRUSGANTVKNQ 20
DB 2 POSIMRANGATVKNQ 20

RESULT 10
QY98M8 PRELIMINARY; PRT, 324 AA.
AC Q23801
DT 02/1981/1998 (ITEMBELrel. 05; Created)
DT 01-JAN-1998 (ITEMBELrel. 05; Last annotation update)
DT 01-MAR-2002 (ITEMBELrel. 20; Last annotation update)
DB Ananas comosus (Pineapple)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae; Incaeae sedis;
OC Nymphaeales; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae;
OC NCBT_TaxID=4615;
RN NCBT_TaxID=4615;
RP SEQUENCE FROM N.A.
RC STAIN=CV; N67-10; TISSUE=FRUIT;
RA Mula E., Osamio Y., Oca S.,
EL Submitted (07-1994) to the EMBL/GenBank/DBJ databases.
DB EMBL; D98334; BA02546.1; ..

DR MEROPS; C01.002;
DR InterPro: IP000169; SHPoc_aseite.
DR ProDom: PD000158; Peptidase Cl.
DR ProDom: PD000158; Peptidase Cl.
DR PROSITE; PS00119; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_ASN; 1.
FT CHAIN 1
FT CDS 95..312
SQ SEQUENCE 324 AA; 36038 MW; 05746C594439F CDS64.
Query Match Similarity 80.0%; Score 84; DB 10; Length 324;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPOSIMRUSGANTVKNQ 19
DB 96 VPOSIMRANGATVKNQ 114

RESULT 11
QY98M8 PRELIMINARY; PRT, 337 AA.
AC Q83334
DT 01-JUN-2002 (ITEMBELrel. 21; Created)
DT 01-JUN-2002 (ITEMBELrel. 21; Last annotation update)
DT 01-JUN-2002 (ITEMBELrel. 21; Last annotation update)
DB Cysteine protease.
OS Lycopersicon pennellii (Tomato)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asteridiales; eudicotyledons; Solanales; Solanaceae; Solanum
RP SEQUENCE FROM N.A.
RX PubMed=1976458;
RA Mulder S., Jones J.M.,
ET 'A Tomato Cysteine Protease Required for CE-2-Dependent Disease
Resistance and Suppression of Autonecrosis'.
DB EMBL; AF492333; AAM19208.1; ..
SQ SEQUENCE 337 AA; 37389 MW; CE7684455656FBE CDS64.

Query Match Similarity 80.0%; Score 84; DB 10; Length 337;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPOSIMRUSGANTVKNQ 20
DB 123 MGSIMRANGATVKNQ 142

RESULT 12
QY98M8 PRELIMINARY; PRT, 351 AA.
AC Q23791
DT 02/1981/1998 (ITEMBELrel. 05; Created)
DT 01-JAN-1998 (ITEMBELrel. 05; Last annotation update)
DT 01-MAR-2002 (ITEMBELrel. 20; Last annotation update)
DB Ananas comosus (Pineapple)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae; Incaeae sedis;
OC Nymphaeales; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae; Nymphaeaceae;
OC NCBT_TaxID=4615;
RN NCBT_TaxID=4615;
RP SEQUENCE FROM N.A.

GenData version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 16:06:14 / Search time 25 seconds

164,838 Million cell updates/sec

Hit: us-09-674-738-1

Perfect score: 198

Sequence: 1 VP08IDMRGCVATSYNKN 20

Scoring table: BLOSUM62

Gap: 10.0, Gapext: 0.5

Search: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Collecting limit 45 summaries

Database: 1: SPRENBL_21.*

- 2: sp:actin
- 3: sp:actin
- 4: sp:actin
- 5: sp:actin
- 6: sp:actin
- 7: sp:actin
- 8: sp:actin
- 9: sp:actin
- 10: sp:actin
- 11: sp:actin
- 12: sp:actin
- 13: sp:actin
- 14: sp:actin
- 15: sp:actin
- 16: sp:actin
- 17: sp:actin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB ID	Description
1	108	100.0	10	10	095965	095965 anas com
2	108	100.0	356	10	081084	081084 anas com
3	108	100.0	356	10	081084	081084 anas com
4	108	100.0	356	10	081084	081084 anas com
5	99	91.7	30	10	021921	021921 anas com
6	97	88.8	20	10	095965	095965 anas com
7	97	88.8	20	10	095965	095965 anas com
8	92	85.2	357	10	081085	081085 anas com
9	90	83.3	340	10	021890	021890 anas com
10	90	83.3	340	10	021890	021890 anas com
11	80	74.1	454	5	095967	095967 anas bi
12	80	74.1	454	5	095967	095967 anas bi
13	79	73.1	344	10	095965	095965 anas bi
14	79	73.1	344	10	095965	095965 anas bi
15	77	71.3	311	5	095966	095966 anas bi
16	77	71.3	311	5	095966	095966 anas bi

17	71.3	317	5	095959	095959 della indic
18	71.3	317	5	095959	095959 della indic
19	70.4	227	10	095918	095918 carica papa
20	70.4	352	10	095911	095911 carica papa
21	70.4	352	10	095911	095911 carica papa
22	70.4	352	10	095911	095911 carica papa
23	70.4	352	10	095911	095911 carica papa
24	70.4	352	10	095911	095911 carica papa
25	70.4	352	10	095911	095911 carica papa
26	70.4	352	10	095911	095911 carica papa
27	69.4	169	5	095957	095957 anas bi
28	69.4	169	5	095957	095957 anas bi
29	69.4	169	5	095957	095957 anas bi
30	69.4	169	5	095957	095957 anas bi
31	69.4	169	5	095957	095957 anas bi
32	69.4	169	5	095957	095957 anas bi
33	69.4	169	5	095957	095957 anas bi
34	69.4	169	5	095957	095957 anas bi
35	69.4	169	5	095957	095957 anas bi
36	69.4	169	5	095957	095957 anas bi
37	69.4	169	5	095957	095957 anas bi
38	69.4	169	5	095957	095957 anas bi
39	69.4	169	5	095957	095957 anas bi
40	69.4	169	5	095957	095957 anas bi
41	69.4	169	5	095957	095957 anas bi
42	69.4	169	5	095957	095957 anas bi
43	69.4	169	5	095957	095957 anas bi
44	69.4	169	5	095957	095957 anas bi
45	69.4	169	5	095957	095957 anas bi

ALIGNMENTS

RESULT 1
095965 PRELIMINARY: PRT: 20 AA.

1: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
2: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
3: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
4: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
5: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
6: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
7: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
8: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
9: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
10: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
11: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
12: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
13: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
14: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
15: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
16: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
17: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
18: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
19: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
20: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
21: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
22: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
23: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
24: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
25: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
26: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
27: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
28: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
29: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
30: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
31: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
32: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
33: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
34: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
35: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
36: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
37: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
38: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
39: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
40: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
41: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
42: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
43: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
44: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)
45: us-09-674-738-1 (us-09-674-738-1) (us-09-674-738-1)

Query Match: 100.0% Score 198, DB 10, Length 20,
Identical: 100.0% Predicted No. 7, 1e-11, Mismatches 0, Indels 0, Gaps 0,
Matches 20, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

DB: 1 VP08IDMRGCVATSYNKN 20

RESULT 2
081084 PRELIMINARY: PRT: 356 AA.

AC: 081084 (us-09-674-738-1) (us-09-674-738-1)
DT: 01-NOV-1998 (us-09-674-738-1) (us-09-674-738-1)

0.

Search completed: November 21, 2002, 16:09:59
Job time : 27 secs

GenCode version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 16:07:14 | Search time 13 Seconds
(without alignment)

147,899 Million cell updates/sec

Title: US-09-674-738-2

Perfect score: 105

Sequence: 1 VSQSDIMDSQAVTSVNNQGS 20

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 28322 seqs, 3513422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Matching filter is: minimize

Database:

1: p17_1*

2: p17_2*

3: p17_3*

4: p17_4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	105	100.0	35	1	VSQSDIMDSQAVTSVNNQGS 20
2	105	100.0	35	2	VSQSDIMDSQAVTSVNNQGS 20
3	105	100.0	35	3	VSQSDIMDSQAVTSVNNQGS 20
4	105	100.0	35	4	VSQSDIMDSQAVTSVNNQGS 20
5	105	100.0	35	5	VSQSDIMDSQAVTSVNNQGS 20
6	105	100.0	35	6	VSQSDIMDSQAVTSVNNQGS 20
7	105	100.0	35	7	VSQSDIMDSQAVTSVNNQGS 20
8	105	100.0	35	8	VSQSDIMDSQAVTSVNNQGS 20
9	105	100.0	35	9	VSQSDIMDSQAVTSVNNQGS 20
10	105	100.0	35	10	VSQSDIMDSQAVTSVNNQGS 20
11	105	100.0	35	11	VSQSDIMDSQAVTSVNNQGS 20
12	105	100.0	35	12	VSQSDIMDSQAVTSVNNQGS 20
13	105	100.0	35	13	VSQSDIMDSQAVTSVNNQGS 20
14	105	100.0	35	14	VSQSDIMDSQAVTSVNNQGS 20
15	105	100.0	35	15	VSQSDIMDSQAVTSVNNQGS 20
16	105	100.0	35	16	VSQSDIMDSQAVTSVNNQGS 20
17	105	100.0	35	17	VSQSDIMDSQAVTSVNNQGS 20
18	105	100.0	35	18	VSQSDIMDSQAVTSVNNQGS 20
19	105	100.0	35	19	VSQSDIMDSQAVTSVNNQGS 20
20	105	100.0	35	20	VSQSDIMDSQAVTSVNNQGS 20
21	105	100.0	35	21	VSQSDIMDSQAVTSVNNQGS 20
22	105	100.0	35	22	VSQSDIMDSQAVTSVNNQGS 20
23	105	100.0	35	23	VSQSDIMDSQAVTSVNNQGS 20
24	105	100.0	35	24	VSQSDIMDSQAVTSVNNQGS 20
25	105	100.0	35	25	VSQSDIMDSQAVTSVNNQGS 20
26	105	100.0	35	26	VSQSDIMDSQAVTSVNNQGS 20
27	105	100.0	35	27	VSQSDIMDSQAVTSVNNQGS 20
28	105	100.0	35	28	VSQSDIMDSQAVTSVNNQGS 20
29	105	100.0	35	29	VSQSDIMDSQAVTSVNNQGS 20

30	80	74.2	415	2	GSE6232	Cysteine proteases
31	80	74.2	471	1	KRR208	Cysteine proteases
32	79	75.2	321	2	AS9040	Cysteine proteases
33	79	75.2	345	1	PERP	Cysteine proteases
34	79	75.2	345	1	PERP	Cysteine proteases
35	79	75.2	354	2	GSE6232	Cysteine proteases
36	79	75.2	354	2	GSE6232	Cysteine proteases
37	79	75.2	371	2	GSE6232	Cysteine proteases
38	79	75.2	371	2	GSE6232	Cysteine proteases
39	79	75.2	371	2	GSE6232	Cysteine proteases
40	79	75.2	371	2	GSE6232	Cysteine proteases
41	78	74.3	358	2	UC7787	Cysteine proteases
42	78	74.3	358	2	UC7787	Cysteine proteases
43	78	74.3	358	2	UC7787	Cysteine proteases
44	78	74.3	358	2	UC7787	Cysteine proteases
45	78	74.3	358	2	UC7787	Cysteine proteases

ALIGNMENTS

RESULT 1

846204 (EC 3.4.22.11) (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

VSQSDIMDSQAVTSVNNQGS 20 (pinapple, fragment)

QY 1 VP02IDM0G0ATSVYVNG 20
 123 LPSIDM0K0ATSVYVNG 151

RESULT 8

Fruit bromelain (EC 3.4.22.33) P11035 precursor - pineapple (fragment)

C/Spectrum: Ananas comosus (pineapple)
 C/Dates: 16-Jul-1999 (sequence revision 16-Jul-1999) (text-change 20-Jun-2000)

R/Comments: 11053
 R/Status: E; Okamoto, Y.; Oda, S.

submitted to the EMBL Data Library, October 1994

A/Accession: J11053
 A/Reference number: J11065

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:D38524

C/Superfamily: papain
 C/Keywords: cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

Query Match 80.0% Score 84; DB 2; Length 334;
 Best Local Similarity 84.2% Pred. No. 4.4e-06;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VP02IDM0G0ATSVYVNG 19
 DB 96 VP02IDM0G0ATSVYVNG 114

RESULT 9

Fruit bromelain (EC 3.4.22.33) P11035 precursor - pineapple

C/Spectrum: Ananas comosus (pineapple)
 C/Dates: 16-Jul-1999 (sequence revision 16-Jul-1999) (text-change 20-Jun-2000)

R/Comments: 11053
 R/Status: E; Okamoto, Y.; Oda, S.

submitted to the EMBL Data Library, January 1995

A/Accession: J11053
 A/Reference number: J11060

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:D14059

C/Superfamily: papain
 C/Keywords: cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

Query Match 80.0% Score 84; DB 2; Length 331;
 Best Local Similarity 84.2% Pred. No. 4.4e-06;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VP02IDM0G0ATSVYVNG 19
 DB 123 VP02IDM0G0ATSVYVNG 141

RESULT 10

Fruit bromelain (EC 3.4.22.33) P11035 precursor - pineapple

C/Spectrum: Ananas comosus (pineapple)
 C/Dates: 16-Jul-1999 (sequence revision 16-Jul-1999) (text-change 20-Jun-2000)

R/Comments: 11053
 R/Status: E; Okamoto, Y.; Oda, S.

submitted to the EMBL Data Library, October 1994

A/Accession: J11053
 A/Reference number: J11065

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:D38524

C/Superfamily: papain
 C/Keywords: cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

chymopapain (EC 3.4.22.6) precursor (unlabeled) - papaya

C/Spectrum: Carica papaya (papaya)
 C/Dates: 16-Jul-1999 (sequence revision 16-Jul-1999) (text-change 18-Aug-2000)

R/Comments: 109760
 R/Status: I; F.; Saito, S.

submitted to the EMBL Data Library, May 1996

A/Accession: J09760
 A/Reference number: J09760

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:X9783; NID-g132460; PID-g132461

A/Superfamily: source: leaf
 A/Keywords: papain, cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

Query Match 80.0% Score 84; DB 2; Length 352;
 Best Local Similarity 84.2% Pred. No. 4.4e-06;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 POSIDM0G0ATSVYVNG 20
 DB 136 POSIDM0G0ATSVYVNG 154

RESULT 11

chymopapain L (EC 3.4.22.6) precursor - papaya

C/Spectrum: Carica papaya (papaya)
 C/Dates: 16-Oct-1996 (sequence revision 16-Oct-1996) (text-change 22-Jun-1999)

R/Comments: 109760
 R/Status: I; F.; Saito, S.

submitted to the EMBL Data Library, May 1996

A/Accession: J09760
 A/Reference number: J09760

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:X9783; NID-g132460; PID-g132461

A/Superfamily: source: leaf
 A/Keywords: papain, cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

Query Match 80.0% Score 84; DB 2; Length 352;
 Best Local Similarity 84.2% Pred. No. 4.4e-06;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 POSIDM0G0ATSVYVNG 20
 DB 136 POSIDM0G0ATSVYVNG 154

RESULT 12

chymopapain L (EC 3.4.22.6) precursor - papaya

C/Spectrum: Carica papaya (papaya)
 C/Dates: 16-Oct-1996 (sequence revision 16-Oct-1996) (text-change 22-Jun-1999)

R/Comments: 109760
 R/Status: I; F.; Saito, S.

submitted to the EMBL Data Library, May 1996

A/Accession: J09760
 A/Reference number: J09760

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:X9783; NID-g132460; PID-g132461

A/Superfamily: source: leaf
 A/Keywords: papain, cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

Query Match 80.0% Score 84; DB 2; Length 352;
 Best Local Similarity 84.2% Pred. No. 4.4e-06;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 POSIDM0G0ATSVYVNG 20
 DB 136 POSIDM0G0ATSVYVNG 154

RESULT 13

chymopapain L (EC 3.4.22.6) precursor - papaya

C/Spectrum: Carica papaya (papaya)
 C/Dates: 16-Oct-1996 (sequence revision 16-Oct-1996) (text-change 22-Jun-1999)

R/Comments: 109760
 R/Status: I; F.; Saito, S.

submitted to the EMBL Data Library, May 1996

A/Accession: J09760
 A/Reference number: J09760

A/Molecule type: mRNA
 A/Notes: precursor translated from GB/BMBL/DB03

A/Residues: 1-324 <MT>
 A/Cross-references: BMBL:X9783; NID-g132460; PID-g132461

A/Superfamily: source: leaf
 A/Keywords: papain, cysteine proteinase, hydrolase

F.110-324/Domain: catalytic domain, predicted <MT>
 F.110-252-273/Active site: Cys, His, Asn residues predicted

Query Match 80.0% Score 84; DB 2; Length 352;
 Best Local Similarity 84.2% Pred. No. 4.4e-06;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 POSIDM0G0ATSVYVNG 20
 DB 136 POSIDM0G0ATSVYVNG 154

Query Match 86.1% Score 63 DB 2 Length 20;
Best Local Similarity 94.7% Pred. No. 14e-08;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;
QY 1 VP0SIDMBDQVATVSNK 19
DB 1 VP0SIDMBDQVATVSNK 19

RESULT 6

anasin (EC 3.4.22.31) precursor - pineapple
C|Species: Ananas comosus (pineapple)
C|Date: 14-May-1999 sequence, revision 14-May-1999 fixec_change 20-Jun-2000
R|Robertson, C.E.; Goodenough, P.M.
submitted to the EMBL data library, November 1997
A|Accession: T07819
A|Molecule type: cDNA
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Residues: 1-345 <DB>
A|Cross-references: EMBL:A000477; FIDM:CA00467.1
A|Gene: ANI
C|Superfamily: papain
C|Description: hydrolyzes proteins with broad specificity; cysteine proteinase
F1:24/Domain1: signal sequence Hecatus predicted <SIG>
F1:25-345/Product: anasin Hecatus predicted <MT>
F1:57-275/300/Active site: Cys, His, Asn Hecatus predicted
Query Match 86.1% Score 93 DB 2 Length 345;
Best Local Similarity 94.7% Pred. No. 3.2e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VP0SIDMBDQVATVSNK 19
DB 123 VP0SIDMBDQVATVSNK 141

RESULT 9

anasin (EC 3.4.22.31) precursor: ANI - pineapple
C|Species: Ananas comosus (pineapple)
C|Date: 14-May-1999 sequence, revision 14-May-1999 fixec_change 20-Jun-2000
R|Robertson, C.E.; Goodenough, P.M.
submitted to the EMBL data library, July 1998
A|Accession: T07819
A|Molecule type: cDNA
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Residues: 1-357 <DB>
A|Cross-references: EMBL:A000830; FIDM:CA00861.1
A|Gene: anil
C|Superfamily: papain
C|Description: hydrolyzes proteins with broad specificity; cysteine proteinase
F1:24/Domain1: signal sequence Hecatus predicted <SIG>
F1:25-357/Product: anasin ANI Hecatus predicted <MT>
F1:57-281/300/Active site: Cys, His, Asn Hecatus predicted
Query Match 85.2% Score 92 DB 2 Length 357;
Best Local Similarity 94.4% Pred. No. 5e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VP0SIDMBDQVATVSN 18
DB 123 VP0SIDMBDQVATVSN 140

RESULT 10

fruit bromelain (EC 3.4.22.3) m92 precursor - pineapple (fragment)
C|Species: Ananas comosus (pineapple)
C|Date: 16-Jul-1999 sequence, revision 16-Jul-1999 fixec_change 20-Jun-2000
C|Accession: T10516
C|Date: 16-Jul-1999 Y. Ota, S.
submitted to the EMBL data library, October 1994
A|Accession: T10516
A|Molecule type: cDNA
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Residues: 1-152 <DB>
A|Cross-references: EMBL:D28513
A|Experimental source: cv. N67-10; nearly mature fruit
A|Description: hydrolyzes proteins with broad specificity; cysteine proteinase
C|Superfamily: papain
C|Description: hydrolyzes proteins; hydrolyase
F1:24/Domain1: signal sequence Hecatus predicted <SIG>
F1:25-117/Domain1: asio-termain propetide Hecatus predicted <MT>
F1:27-287/300/Active site: Cys, His, Asn Hecatus predicted
Query Match 89.3% Score 90 DB 2 Length 340;
Best Local Similarity 93.1% Pred. No. 1e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 VP0SIDMBDQVATVSNK 20
DB 123 VP0SIDMBDQVATVSNK 142

RESULT 11

fruit bromelain (EC 3.4.22.3) p93 precursor - pineapple
C|Species: Ananas comosus (pineapple)
C|Date: 16-Jul-1999 sequence, revision 16-Jul-1999 fixec_change 20-Jun-2000
R|Noto Eom, Azeaki, H.; Takai, Y.; Kono, A.; Okamoto, Y.; Ota, S.
submitted to the EMBL data library, January 1993
A|Accession: T10501
A|Molecule type: cDNA
A|Status: translated from GB/EMBL/DBJ
A|Residues: 1-352 <MT>
A|Cross-references: EMBL:D10508
A|Experimental source: cv. N67-10; fruit; nearly mature
A|Description: hydrolyzes proteins; cysteine proteinase
C|Superfamily: papain
C|Description: hydrolyzes proteins; hydrolyase
F1:24/Domain1: asio-termain propetide Hecatus predicted <SIG>
F1:25-152/Domain1: catboxy-termain propetide Hecatus predicted <CTP>
F1:57-281/300/Active site: Cys, His, Asn Hecatus predicted
Query Match 89.3% Score 90 DB 2 Length 352;
Best Local Similarity 89.0% Pred. No. 1e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 VP0SIDMBDQVATVSNK 20
DB 124 VP0SIDMBDQVATVSNK 143

RESULT 12

JC4848
cysteine proteinase (EC 3.4.22.-) - Douglas Elm

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Search completed: November 21, 2002, 16:10:31
Job time : 14 secs

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Search completed: November 21, 2002, 16:10:31
Job time : 14 secs

GenScope Version 5.1.3
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OK Protein - protein search using sw model

Run on: November 21, 2002, 16:07:39, Search time 11.5 seconds

Weight alignment 51.170 Million cell updates/sec

Title: US-09-674-738-1

Parent score: 108

Sequence: 1 VP52IRGQVAVSNQK 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942322 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 260000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing files: 45 summaries

Prod. No. is the number of results predicted by a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

DATABASES

Result Query Query Length DB ID Description

1	108	100.0	213	2	US-08-578-701A-1	Sequence 1, Appl 1
2	108	100.0	213	2	US-08-578-701A-1	Sequence 1, Appl 1
3	88	81.5	18	4	US-09-318-689A-1	Sequence 1, Appl 1
4	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
5	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
6	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
7	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
8	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
9	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
10	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
11	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
12	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
13	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
14	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
15	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
16	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
17	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
18	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
19	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
20	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
21	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
22	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
23	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
24	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
25	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
26	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1
27	79	73.1	127	4	US-09-318-932A-1	Sequence 1, Appl 1

ALIGNMENTS

Result 1

US-09-674-738-1

Sequence 1, Application US/6578701A

Parent No. 584105

Appl No. 584105

Appl Name: M9021

Appl Desc: M9021

Appl Desc: M9021

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Appl Desc: M9021

28	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
29	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
30	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
31	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
32	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
33	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
34	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
35	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
36	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
37	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
38	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
39	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
40	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
41	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
42	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
43	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
44	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1
45	72	66.7	220	4	US-08-578-701A-1	Sequence 85, Appl 1

Query Match 100.0%, Score 108, DB 21, Length 213,
Best Local Similarity 100.0%, Pred. No. 9.5e11,
Matches 20, Conservative 0, Mismatches 0, Gaps 0,
By 1 VP52IRGQVAVSNQK 20
2 VP52IRGQVAVSNQK 21

```

RESULT 2
US-08-360-693-1
; PRIOR APPLICATION NUMBER: US/06360693
; Patent No. 592640
; GENERAL INFORMATION:
; TITLE OF INVENTION: Tissue
; TITLE OF INVENTION: USE OF ENZYMES, ESPECIALLY BROMELAIN, IN
; NUMBER OF INVENTIONS: THE TREATMENT OF DIARRHEA
; NUMBER OF INVENTIONS:
; ADDRESSES: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: COMPAQ DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 08/360,693
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: A24
; PRIOR APPLICATION NUMBER: WO PCT/GB93/01374
; FILING DATE: 30-JUN-1993
; APPLICATION NUMBER: GB 931389.4
; FILING DATE: 25-JUN-1993
; PRIOR APPLICATION DATA: GB 9308164.4
; FILING DATE: 20-APR-1993
; PRIOR APPLICATION DATA: GB 9313862.7
; FILING DATE: 30-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 30357/115/KIST
; TELEPHONE: (202) 675-5000
; TELEFAX: (202) 672-5399
; TELETYPE:
; INFORMATION ID NO. 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-360-693-1
Query Match 100.0%; Score 108; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 9,5e-11;
Matches 40; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQSDIMRWGVATSVNQN 20
DB 2 VQSDIMRWGVATSVNQN 21

RESULT 3
US-09-32-689A-1
; PRIOR APPLICATION NUMBER: US/0932689A
; Patent No. 635542
; GENERAL INFORMATION:
; APPLICANT: Mykott, Tracy Lehmanne
; APPLICANT: Peak, Keith
; TITLE OF INVENTION: Component of Bromelain
; CURRENT APPLICATION NUMBER: US/09382689A

US-09-32-689A-1
Query Match 100.0%; Score 88; DB 4; Length 18;
Best Local Similarity 86.9%; Pred. No. 1.1e-08;
Matches 16; Mismatches 2; Indels 0; Gaps 0;

QY 1 VQSDIMRWGVATSVNQN 18
DB 1 VQSDIMRWGVATSVNQN 18

RESULT 4
US-09-32-932A-176
; Sequence 176; Application US/09325932A
; GENERAL INFORMATION:
; APPLICANT: Filmm, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develo
; CURRENT APPLICATION NUMBER: US/09325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: SEQ ID NOS for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 127
; ORGANISM: Eucalyptus grandis
US-09-32-932A-176
Query Match 73.1%; Score 79; DB 4; Length 127;
Best Local Similarity 68.4%; Pred. No. 4.3e-06;
Matches 13; Mismatches 2; Indels 0; Gaps 0;

QY 1 VQSDIMRWGVATSVNQN 19
DB 67 LQVDFDMDGVATSVNQN 95

RESULT 5
US-09-325-932A-167
; Sequence 167; Application US/09325932A
; GENERAL INFORMATION:
; APPLICANT: Filmm, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develo
; CURRENT APPLICATION NUMBER: US/09325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: SEQ ID NOS for Windows Version 3.0
; SEQ ID NO 167
; LENGTH: 148
; ORGANISM: Eucalyptus grandis

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US-09-325-932A-167
Query Match      73.1%  Score 79; DB 4; Length 148;
Best Local Similarity 68.4%; Pred. No. 5,2e-06;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 57 LP05IDMDQVATGYVND 75

RESULT 6
US-09-325-932A-165
Sequence 165; Application US/0935932A
GENERAL INFORMATION:
APPLICANT: plant, hairy
TITLE OF INVENTION: homecellulose affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
FILE REFERENCE: 32290-144749
CURRENT FILING DATE: 1998-07-22
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SEQ ID NO 165
SOFTWARE: Windows Version 3.0
LENGTH: 278
ORGANISM: Baculovirus grandis

US-09-325-932A-165
Query Match      73.1%  Score 79; DB 4; Length 278;
Best Local Similarity 68.4%; Pred. No. 1,2e-05;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 144 LP05IDMDQVATGYVND 162

RESULT 7
US-09-320-365-62
Sequence 62; Application US/09120365
GENERAL INFORMATION:
APPLICANT: natory, shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT FILING DATE: 1998-07-22
CURRENT FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 62
SOFTWARE: Patent In Ver. 2.0
LENGTH: 339
ORGANISM: Sarcophaga cathepsin L

US-09-320-365-62
Query Match      73.1%  Score 79; DB 3; Length 339;
Best Local Similarity 68.4%; Pred. No. 1,5e-05;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 122 VPS0IDMDQVATGYVND 140

RESULT 8
US-09-320-365-80
Sequence 80; Application US/09120365
Patent No. 610314

US-09-325-932A-167
Query Match      73.1%  Score 79; DB 4; Length 148;
Best Local Similarity 68.4%; Pred. No. 5,2e-06;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 57 LP05IDMDQVATGYVND 75

RESULT 6
US-09-325-932A-165
Sequence 165; Application US/0935932A
GENERAL INFORMATION:
APPLICANT: plant, hairy
TITLE OF INVENTION: homecellulose affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
FILE REFERENCE: 32290-144749
CURRENT FILING DATE: 1998-07-22
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SEQ ID NO 165
SOFTWARE: Windows Version 3.0
LENGTH: 278
ORGANISM: Baculovirus grandis

US-09-325-932A-165
Query Match      73.1%  Score 79; DB 4; Length 278;
Best Local Similarity 68.4%; Pred. No. 1,2e-05;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 144 LP05IDMDQVATGYVND 162

RESULT 7
US-09-320-365-62
Sequence 62; Application US/09120365
GENERAL INFORMATION:
APPLICANT: natory, shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT FILING DATE: 1998-07-22
CURRENT FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 62
SOFTWARE: Patent In Ver. 2.0
LENGTH: 339
ORGANISM: Sarcophaga cathepsin L

US-09-320-365-62
Query Match      73.1%  Score 79; DB 3; Length 339;
Best Local Similarity 68.4%; Pred. No. 1,5e-05;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 122 VPS0IDMDQVATGYVND 140

RESULT 8
US-09-320-365-80
Sequence 80; Application US/09120365
Patent No. 610314

US-09-325-932A-167
Query Match      73.1%  Score 79; DB 4; Length 148;
Best Local Similarity 68.4%; Pred. No. 5,2e-06;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 57 LP05IDMDQVATGYVND 75

RESULT 6
US-09-325-932A-165
Sequence 165; Application US/0935932A
GENERAL INFORMATION:
APPLICANT: plant, hairy
TITLE OF INVENTION: homecellulose affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
FILE REFERENCE: 32290-144749
CURRENT FILING DATE: 1998-07-22
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SEQ ID NO 165
SOFTWARE: Windows Version 3.0
LENGTH: 278
ORGANISM: Baculovirus grandis

US-09-325-932A-165
Query Match      73.1%  Score 79; DB 4; Length 278;
Best Local Similarity 68.4%; Pred. No. 1,2e-05;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 144 LP05IDMDQVATGYVND 162

RESULT 7
US-09-320-365-62
Sequence 62; Application US/09120365
GENERAL INFORMATION:
APPLICANT: natory, shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT FILING DATE: 1998-07-22
CURRENT FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 62
SOFTWARE: Patent In Ver. 2.0
LENGTH: 339
ORGANISM: Sarcophaga cathepsin L

US-09-320-365-62
Query Match      73.1%  Score 79; DB 3; Length 339;
Best Local Similarity 68.4%; Pred. No. 1,5e-05;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 VP05IDMDQVATGYVND 19
DB 122 VPS0IDMDQVATGYVND 140

RESULT 8
US-09-320-365-80
Sequence 80; Application US/09120365
Patent No. 610314

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Query Match 73 31; Score 79; DB 4; Length 339;
 Best Local Similarity 69 44; Pred. No. 15e-05;

Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 122 VPOSIDNRGVATVNNQ 140

RESULT 11

US-08-883-526-4

Sequence 4; Application US/08883526

Score 79; DB 4; Length 339;

Best Local Similarity 69 44; Pred. No. 15e-05;

Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 122 VPOSIDNRGVATVNNQ 140

RESULT 12

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 13

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 14

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 15

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 16

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 17

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 18

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 114 VPOSIDNRGVATVNNQ 132

RESULT 19

US-09-120-365-49

Sequence 4; Application US/09120365

Score 75; DB 3; Length 334;

Best Local Similarity 69 44; Pred. No. 9e-05;

APPLICANT: INCOTI, SHUNJI
 TITLE OF INVENTION: NEW PROTEASE
 FILE REFERENCE: 32290-14749
 CURRENT APPLICATION NUMBER: US/09/120,365
 EARLIER APPLICATION NUMBER: JP 9-333 474
 EARLIER FILING DATE: 1997-11-18
 INVENTOR: INCOTI, SHUNJI
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 69
 TYPE: PRT
 ORGANISM: Leishmania
 US-09-120-365-49

Query Match 69 44; Score 75; DB 3; Length 443;
 Best Local Similarity 69 44; Pred. No. 9e-05;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 13

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 14

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 15

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 16

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 17

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 18

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

RESULT 19

US-09-515-039-49

Sequence 4; Application US/09515039

Score 75; DB 3; Length 443;

Best Local Similarity 69 44; Pred. No. 9e-05;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPOSIDNRGVATVNNQ 19

DB 126 VPOSIDNRGVATVNNQ 144

Query Match 68.5% Score 74; DB 3; Length 334;
 Becc Local Similarity 63.2% Pred. No. 0.0001;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 VPOSIDMRCVGAATSYKNO 19
 DB 114 IKSJUMRKCCTPYKNO 132

RESULT 15
 / Sequence 64, Application US/09515039
 / Patent No. 621459
 / ORIGINATOR INFORMATION
 / ORIGINATOR NAME: Snuji
 / TITLE OF INVENTION: NEW PROTENSE
 / FILE REFERENCE: 3238-34449 US/09/515.039
 / CURRENT FILING DATE: 2000-03-06
 / EXPIRY DATE: 2010-03-06
 / EXPIRY APPLICATION NUMBER: JP 9-333 474
 / NUMBER OF SEQ ID NOS: 101
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 64
 / DEFINITION
 / TYPE: PRT
 / ORIGINISM: Murine cathedin L
 / US-09-515-039-64
 Query Match 68.5% Score 74; DB 4; Length 334;
 Becc Local Similarity 63.2% Pred. No. 0.0001;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 VPOSIDMRCVGAATSYKNO 19
 DB 114 IKSJUMRKCCTPYKNO 132

Search completed: November 21, 2002, 16:11:01
 Job time : 12.5 secs



RESULT 2
 US-08-360-693-1
 Application US/08360693
 Patent No. 5928640
 GENERAL INFORMATION:
 INVENTOR: FRANK J.
 TITLE OF INVENTION: USE OF ENZYMES, ESPECIALLY BROMELAIN, IN
 THE TREATMENT OF DIARRHOEA
 NUMBER OF SEQUENCES: 1
 COUNTRY: USA
 ADDRESS: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 900
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 COMPT: 300073109
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 14-FEB-1995
 PRIORITY APPLICATION NUMBER: WO PCT/GB93/01374
 FILING DATE: 30-JUN-1993
 PRIOR APPLICATION DATA: GB 931389.4
 FILING DATE: 25-JUN-1993
 PRIOR APPLICATION DATA: GB 9308164.4
 FILING DATE: 26-APR-1993
 PRIOR APPLICATION NUMBER: GB 9213862.7
 ATTORNEY/AGENT INFORMATION:
 NAME: BENJAMIN STEPHEN A. 9, 768
 REFERENCE/DOCKET NUMBER: 30157/115/ALIST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 472-5390
 TELEFAX: (202) 472-5393
 INVENTOR'S PERSONAL DATA:
 NAME: 904136
 LENGTH: 213 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-360-693-1

Query Match 88.4%; Score 93; DB 3; Length 213;
 Best Local Similarity 94.7%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPQSDIMDSGAVTSVNVQ 19
 Db 2 VPQSDIMDSGAVTSVNVQ 20
 RESULT 3
 US-08-883-526-4
 Application US/08883526
 Patent No. 6059930
 GENERAL INFORMATION:
 INVENTOR: BERNARD, OLGA
 APPLICANT: Queigler, Karl J. C.
 APPLICANT: Shah, Parvati
 TITLE OF INVENTION: NEW HUMAN CATHESPIN
 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 11100 Water Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 COMPT: 94304
 MEDIUM TYPE: Floppy disk
 SOFTWARE: DOS
 OPERATING SYSTEM: DOS
 SOFTWARE: Patented for Windows Version 2.0
 CURRENT APPLICATION DATA:
 FILING DATE: Hereafter
 PRIORITY APPLICATION DATA:
 FILING DATE:
 APPLICATION NUMBER:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115
 TYPE: amino acid
 STRANDNESS: single
 IMMEDIATE SOURCE:
 LIBRARY: 1468964
 CLONE: GenBank
 US-08-883-526-4

Query Match 79.0%; Score 83; DB 3; Length 334;
 Best Local Similarity 70.0%; Pred. No. 1.1e-05;
 Matches 47; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VPQSDIMDSGAVTSVNVQ 20
 Db 114 VPQSDIMDSGAVTSVNVQ 133
 RESULT 4
 US-09-120-365-69
 Application US/09120365
 Patent No. 6103514
 GENERAL INFORMATION:
 TITLE OF INVENTION: NEW PROTEASE
 FILE REFERENCE: 32390-144749
 CURRENT APPLICATION NUMBER: US/09/120,365
 EARLIER FILING DATE: 1997-11-18
 EARLIER APPLICATION NUMBER: JP 9-333 474
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 69
 LENGTH: 413
 TYPE: PPT
 ORGANISM: Leishmania
 US-09-120-365-69

Query Match 79.0%; Score 83; DB 3; Length 443;
 Best Local Similarity 70.0%; Pred. No. 1.1e-05;
 Matches 47; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VPQSDIMDSGAVTSVNVQ 20
 Db 114 VPQSDIMDSGAVTSVNVQ 20

DB 126 VPDANMEKQAVTFVNOG 145

RESULT 5

US-09-515-039-69

Sequence 63, Application US/0951039

Patent No. 6414399

APPLICANT: Nitro, Shunji

TITLE OF INVENTION: NEW PROTEASE

CURRENT APPLICATION NUMBER: US/09515,039

CURRENT FILING DATE: 2000-03-06

EARLIER APPLICATION NUMBER: JP-9-333 474

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 443

TYPE: PROT

US-09-515-039-69

Query Match

Best Local Similarity: 78.11, Score 82, DB 4, Length 443

Matches 14, Conservative 3, Mismatches 3, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 126 VPDANMEKQAVTFVNOG 145

RESULT 6

US-09-325-932A-176

Sequence 17, Application US/09325932A

Patent No. 6451504

APPLICANT: Labman, Amette

TITLE OF INVENTION: Compositions affecting programmed cell

FILE REFERENCE: 102

CURRENT APPLICATION NUMBER: US/09325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: PatSeq for Windows Version 3.0

SEQ ID NO 176

LENGTH: 278

TYPE: PROT

US-09-325-932A-176

Query Match

Best Local Similarity: 78.11, Score 82, DB 4, Length 127

Matches 14, Conservative 3, Mismatches 3, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 67 LPDFDMHQAATFVNOG 86

RESULT 7

US-09-325-932A-167

Sequence 16, Application US/09325932A

Patent No. 6414399

APPLICANT: Nitro, Shunji

TITLE OF INVENTION: NEW PROTEASE

CURRENT APPLICATION NUMBER: US/09515,039

CURRENT FILING DATE: 2000-03-06

EARLIER APPLICATION NUMBER: JP-9-333 474

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 443

TYPE: PROT

US-09-325-932A-167

Query Match

Best Local Similarity: 78.11, Score 82, DB 4, Length 127

Matches 14, Conservative 3, Mismatches 3, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 67 LPDFDMHQAATFVNOG 86

RESULT 8

US-09-325-932A-165

Sequence 15, Application US/09325932A

Patent No. 6414399

APPLICANT: Nitro, Shunji

TITLE OF INVENTION: NEW PROTEASE

CURRENT APPLICATION NUMBER: US/09515,039

CURRENT FILING DATE: 2000-03-06

EARLIER APPLICATION NUMBER: JP-9-333 474

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 443

TYPE: PROT

US-09-325-932A-165

Query Match

Best Local Similarity: 78.11, Score 82, DB 4, Length 127

Matches 14, Conservative 3, Mismatches 3, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 67 LPDFDMHQAATFVNOG 86

NUMBER OF SEQ ID NOS: 206
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 167
LENGTH: 148
TYPE: PROT
ORGANISM: Euclatypus grandis
US-09-325-932A-167

Query Match

Best Local Similarity: 78.11, Score 82, DB 4, Length 148

Matches 14, Conservative 3, Mismatches 3, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 57 LPDFDMHQAATFVNOG 76

RESULT 9

US-09-325-932A-165

Sequence 15, Application US/09325932A

Patent No. 6414399

APPLICANT: Nitro, Shunji

TITLE OF INVENTION: NEW PROTEASE

CURRENT APPLICATION NUMBER: US/09515,039

CURRENT FILING DATE: 2000-03-06

EARLIER APPLICATION NUMBER: JP-9-333 474

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 443

TYPE: PROT

US-09-325-932A-165

Query Match

Best Local Similarity: 78.11, Score 82, DB 4, Length 278

Matches 14, Conservative 3, Mismatches 4, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 144 LPDFDMHQAATFVNOG 163

RESULT 10

US-09-325-932A-165

Sequence 15, Application US/09325932A

Patent No. 6414399

APPLICANT: Nitro, Shunji

TITLE OF INVENTION: NEW PROTEASE

CURRENT APPLICATION NUMBER: US/09515,039

CURRENT FILING DATE: 2000-03-06

EARLIER APPLICATION NUMBER: JP-9-333 474

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 443

TYPE: PROT

US-09-325-932A-165

Query Match

Best Local Similarity: 78.11, Score 82, DB 3, Length 134

Matches 13, Conservative 3, Mismatches 3, Indels 0, Gaps 0

CV 1 VPDANMEKQAVTFVNOG 20

DB 114 IPEVDMHQAATFVNOG 133


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RESULT 15
US-09-325-932A-153
/ PUBLISHED IN: Application US/0935932A
/ PUBLICATION NO: 4454104
/ GENERAL INFORMATION:
/ APPLICANT: Film, Batey
/ INVENTOR: James, Mark
/ TITLE OF INVENTION: Compositions affecting programmed cell
/ TITLE OF INVENTION: death and their use in the modification of forestry plant develo
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ. ID NOS.: 206
/ SOURCE: Genbank
/ RELEASED FOR: Windows Version 3.0
/ SEQ ID NO 153
/ LENGTH: 396
/ TYPE: Coding
/ ORGANISM: Pinus radiata
US-09-325-932A-153

Query Match 77.1%, Score 81, Ds 4, Length 396:
Beat Local Similarity 70.0%, Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0.

OY 1 VPSIDWDSGATVSVAQ 20
DB 160 LREIDWMDKDNVYVQ 179

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Search completed: November 21, 2002, 16:11:01
 CPU time : 11.9 secs

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OW protein - protein search, using sw model

Run on: November 21, 2002, 16:06:44 / Search time 117.5 seconds

(without alignments)

Title: US-09-674-738-1

Sequence: 1 VQSIQDNGVATSYNNK 20

Scoring table: Gapco 10.0, Gapex 0.5

Searched: 456344 seqs, 64673110 residues

Total number of hits satisfying chosen parameters: 456344

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing 118745 hits summaries

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5: /cgn2_6/p/cdataa1/pa/US09 COMB pep.*
6: /cgn2_6/p/cdataa1/pa/US09 COMB pep.*
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27: /cgn2_6/p/cdataa1/pa/US09 COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	21	US-09-382-685A.2	Sequence 2, App1
2	108	100.0	21	US-09-382-685A.2	Sequence 3, App1
3	108	100.0	21	US-09-382-685A.2	Sequence 4, App1
4	108	100.0	21	US-09-382-685A.2	Sequence 5, App1
5	108	100.0	21	US-09-382-685A.2	Sequence 6, App1
6	108	100.0	21	US-09-382-685A.2	Sequence 7, App1

108	100.0	356	21	US-09-791-537-86882	Sequence 84882, A
99	91.7	311	21	US-09-743-987-16	Sequence 20, App1
9	91.7	324	21	US-09-743-987-20	Sequence 20, App1
10	91.7	324	21	US-09-743-987-20	Sequence 122, App1
11	91.7	324	21	US-09-743-987-18324	Sequence 84890, A
12	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
13	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
14	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
15	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
16	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
17	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
18	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
19	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
20	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
21	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
22	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
23	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
24	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
25	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
26	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
27	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
28	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
29	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
30	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
31	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
32	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
33	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
34	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
35	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
36	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
37	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
38	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
39	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
40	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
41	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
42	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
43	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
44	91.7	351	21	US-09-791-537-86889	Sequence 84890, A
45	91.7	351	21	US-09-791-537-86889	Sequence 84890, A

ALIGNMENTS

RESULT 1
US-09-674-738-1
Sequence 1
Application US/09674738
APPLICANT: UNAPHARM Arzneimittel GmbH
TITLE OF INVENTION: Use of Bromelain Proteases for Inhibiting Blood
FILE REFERENCE: 08054
CURRENT APPLICATION NUMBER: US/0674 738
CURRENT FILING DATE: 2000-10-31
PRIORITY DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1: catenin ver. 2.1
LENGTH: 20
SEQ ID NO 2: catenin ver. 2.1
US-09-674-738-1
US-09-674-738-1

Query Match	100.0%	Score 108	DB 20	Length 20
Best Local Similarity	100.0%	Pred No. 6	10	
Matches	20	Mismatches	0	Indels 0
1	VQSIQDNGVATSYNNK 20			
1	VQSIQDNGVATSYNNK 20			

REFERENCE/DOCKET NUMBER: 9316
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (1516) 742-1443
 TELEFAX: (1516) 742-1443
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 NO. OF RESIDUES: 356
 US-08-244-796-15

Query Match Score 108 DB 6 Length 212;
 Best Local Similarity 100.0%; Pctd No. 9, 1e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 108 DB 6 Length 212;
 Best Local Similarity 100.0%; Pctd No. 9, 1e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-791-537-84882
 RESULT 6
 US-09-791-537-84882 Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Biomech, Inc.
 APPLICANT: Biomech, Inc.
 APPLICANT: Danese, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 FILE REFERENCE: 261/115
 CURRENT FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: US/09/791,537
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 84879
 LENGTH: 356
 TYPE: PRT
 ORGANISM: Ananas comosus
 US-09-791-537-84879

Query Match Score 108 DB 21 Length 356;
 Best Local Similarity 100.0%; Pctd No. 1, 6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 108 DB 21 Length 356;
 Best Local Similarity 100.0%; Pctd No. 1, 6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-791-537-84882
 RESULT 7
 US-09-791-537-84882 Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Biomech, Inc.
 APPLICANT: Biomech, Inc.
 APPLICANT: Danese, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 FILE REFERENCE: 261/210
 CURRENT FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: US/09/791,537
 NUMBER OF SEQ ID NOS: 157095
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 84882
 LENGTH: 356
 TYPE: PRT
 ORGANISM: Ananas comosus
 US-09-791-537-84882

Query Match Score 108 DB 21 Length 356;
 Best Local Similarity 100.0%; Pctd No. 1, 6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 99 DB 21 Length 311;
 Best Local Similarity 99.1%; Pctd No. 2, 4e-07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match Score 99 DB 21 Length 311;
 Best Local Similarity 99.1%; Pctd No. 2, 4e-07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-743-987-16
 RESULT 8
 US-09-743-987-16 Application US/09743987
 GENERAL INFORMATION:
 APPLICANT: Wyott, Tracy Lahnne
 APPLICANT: Wyott, Tracy Lahnne
 APPLICANT: Wyott, Tracy Lahnne
 TITLE OF INVENTION: CROCKET, BEN CROCKET, BEN CROCKET, BEN CROCKET AND PROTEINS FROM PINKAPPLE STEM
 FILE REFERENCE: 0623 0980000
 CURRENT APPLICATION NUMBER: US/09/743,987
 PRIOR APPLICATION NUMBER: PCT/GB99/02784
 PRIOR FILING DATE: 1999-08-24
 PRIOR APPLICATION NUMBER: GB 9819138
 NUMBER OF SEQ ID NOS: 92
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 311
 LENGTH: 311
 TYPE: PRT
 ORGANISM: Ananas comosus
 US-09-743-987-16

Query Match Score 99 DB 21 Length 311;
 Best Local Similarity 99.1%; Pctd No. 2, 4e-07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match Score 99 DB 21 Length 311;
 Best Local Similarity 99.1%; Pctd No. 2, 4e-07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-743-987-20
 RESULT 9
 US-09-743-987-20 Application US/09743987
 GENERAL INFORMATION:
 APPLICANT: Wyott, Tracy Lahnne
 APPLICANT: Wyott, Tracy Lahnne
 APPLICANT: Wyott, Tracy Lahnne
 TITLE OF INVENTION: CROCKET, BEN CROCKET, BEN CROCKET, BEN CROCKET AND PROTEINS FROM PINKAPPLE STEM
 FILE REFERENCE: 0623 0980000
 CURRENT APPLICATION NUMBER: US/09/743,987
 PRIOR APPLICATION NUMBER: PCT/GB99/02784
 PRIOR FILING DATE: 1999-08-24
 PRIOR APPLICATION NUMBER: GB 9819138
 NUMBER OF SEQ ID NOS: 92
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 324
 LENGTH: 324
 TYPE: PRT
 ORGANISM: Ananas comosus
 US-09-743-987-20

Query Match Score 99 DB 21 Length 344;
 Best Local Similarity 99.1%; Pctd No. 2, 4e-07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match Score 99 DB 21 Length 344;
 Best Local Similarity 99.1%; Pctd No. 2, 4e-07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-791-537-69322
 RESULT 10
 US-09-791-537-69322 Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Biomech, Inc.
 APPLICANT: Biomech, Inc.
 APPLICANT: Danese, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 FILE REFERENCE: 261/210
 CURRENT FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: US/09/791,537
 NUMBER OF SEQ ID NOS: 157095
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 69322
 LENGTH: 356
 TYPE: PRT
 ORGANISM: Ananas comosus
 US-09-791-537-69322

Query Match Score 108 DB 21 Length 356;
 Best Local Similarity 100.0%; Pctd No. 1, 6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Nov 25 08:17:50 2002

us-09-674-738-1. rapm

Page 5

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; SEQ ID NO 5
; LENGTH: 20
; TYPE: PR1
; ORGANISM: Ananas comosus
US-09-382-698-5

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Db      1  VPSIDIMNNGATSVXNO  19

Query Match: 99.8%  Score 97  DB 17  Length 20:
Best Local Similarity 84.7%  Pred. No. 4.2e-08:
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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US-09-750-210A-5
SEQUENCE NUMBER: 09704251.0
APPLICATION: US/09705210A
INVENTOR: Mynott, Tracy Lehman
APPLICANT: Mynott, Tracy Lehman
ATTORNEY: Bowers, Charles
TITLE OF INVENTION: Component of Bromelain
FILE REFERENCE: 063,9740001
CURRENT FILING DATE: US/063/974,010A
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: US/09/382,468
PRIOR FILING DATE: 1997-02-26/CGB6/00590
PRIOR APPLICATION NUMBER: GB 9704251.7
PRIOR FILING DATE: 1997-02-26
PRIOR APPLICATION NUMBER: GB 9704119.6
PRIOR FILING DATE: 1997-02-26
PRIOR APPLICATION NUMBER: GB 9704251.7
PRIOR FILING DATE: 1997-02-26
PRIOR APPLICATION NUMBER: GB 9703827.7
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Piletrin Ver. 2.0
SEQ ID NO: 20
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TYPE: PRT
ORGANISM: ORGANISM: Acanthaceae
US-09-750-210A-5
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2 YGSGIDRAGGATGATGATG 19

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Search completed: November 21, 2002, 16:15:42
Job time : 138.5 secs



Query Match 100.0% Score 105; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3,7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VQSIDMDSGAVTSVKNQ 20

DB 1 VQSIDMDSGAVTSVKNQ 20

RESULT 2

US-09-382-688-4
 GENERAL INFORMATION: Application US/09382688A
 APPLICANT: Mycott, Tracy Lehanne
 APPLICANT: Engelhardt, Christian
 APPLICANT: Engelhardt, Christian
 TITLE OF INVENTION: Component of Bromelain
 FILE REFERENCE: 6623.074001
 CURRENT FILING DATE: 1998-08-25
 PRIOR APPLICATION NUMBER: PCT/GB98/00590
 PRIOR FILING DATE: 1997-03-25
 PRIOR APPLICATION NUMBER: GB 9704252.7
 PRIOR FILING DATE: 1997-03-25
 PRIOR APPLICATION NUMBER: GB 9703850.9
 PRIOR FILING DATE: 1997-02-25
 PRIOR FILING DATE: 1997-02-25
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patent in Ver. 2.0
 SEQ ID NO 1
 LENGTH: 20
 TYPE: PNT
 ORGANISM: Ananas comosus

US-09-382-688-4

Query Match 100.0% Score 105; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3,7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VQSIDMDSGAVTSVKNQ 20

DB 1 VQSIDMDSGAVTSVKNQ 20

RESULT 3

US-09-674-738-2
 GENERAL INFORMATION: Application US/09674738
 APPLICANT: USAPHARM Arzneimittel GmbH
 TITLE OF INVENTION: Bromelain Processes for Inhibiting Blood
 FILE REFERENCE: 80034
 CURRENT FILING DATE: 2000-10-31
 PRIOR APPLICATION NUMBER: US/09/674,738
 CURRENT FILING DATE: 2000-10-31
 PRIOR APPLICATION NUMBER: PCT/EP98/04406
 PRIOR FILING DATE: 1998-07-15
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 2
 LENGTH: 20
 TYPE: PNT
 ORGANISM: pine-apple (Bromeliaceae)

US-09-674-738-2

Query Match 100.0% Score 105; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3,7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VQSIDMDSGAVTSVKNQ 20

DB 1 VQSIDMDSGAVTSVKNQ 20

DB 1 VQSIDMDSGAVTSVKNQ 20

RESULT 4

US-09-750-210A-4
 GENERAL INFORMATION: Application US/09750210A
 APPLICANT: Mycott, Tracy Lehanne
 APPLICANT: Engelhardt, Christian
 APPLICANT: Engelhardt, Christian
 TITLE OF INVENTION: Component of Bromelain
 FILE REFERENCE: 6623.074001 US/09750,210A
 CURRENT FILING DATE: 2000-12-29
 PRIOR APPLICATION NUMBER: US 09/382,688
 PRIOR FILING DATE: 1998-08-25
 PRIOR APPLICATION NUMBER: PCT/GB98/00590
 PRIOR FILING DATE: 1997-03-25
 PRIOR APPLICATION NUMBER: GB 9706119.6
 PRIOR FILING DATE: 1997-03-25
 PRIOR APPLICATION NUMBER: GB 9704252.7
 PRIOR FILING DATE: 1997-02-28
 PRIOR APPLICATION NUMBER: GB 9703850.9
 PRIOR FILING DATE: 1997-02-25
 PRIOR APPLICATION NUMBER: GB 9703827.7
 PRIOR FILING DATE: 1997-02-25
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patent in Ver. 2.0
 SEQ ID NO 4
 LENGTH: 20
 TYPE: PNT
 ORGANISM: ORGANISM: Ananas comosus

US-09-750-210A-4

Query Match 100.0% Score 105; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3,7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VQSIDMDSGAVTSVKNQ 20

DB 1 VQSIDMDSGAVTSVKNQ 20

RESULT 5

US-09-791-537-82408
 GENERAL INFORMATION: Application US/09791537
 APPLICANT: Biocatal, Inc.
 APPLICANT: Debe, Derek
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 FILE REFERENCE: 80034
 CURRENT FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 15305
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 82408
 LENGTH: 216
 TYPE: PNT
 ORGANISM: Ananas comosus

US-09-791-537-82408

Query Match 100.0% Score 105; DB 21; Length 216;
 Best Local Similarity 100.0%; Pred. No. 4,9e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VQSIDMDSGAVTSVKNQ 20

DB 1 VQSIDMDSGAVTSVKNQ 20

RESULT 6

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US-09-791-531-8483
/ TITLE OF INVENTION: Component of Bromelain
/ FILE REFERENCE: US/09791537
/ GENERAL INFORMATION:
/ APPLICANT: Biocrom, Inc.
/ APPLICANT: Denzer, Joseph
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
/ FILE REFERENCE: US/09791537
/ CURRENT FILING DATE: 1997-02-28
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9704552.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 4
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-791-531-8483
Query Match 100.0%; Score 105; DB 21; Length 345;
Match Local Similarity 100.0%; Pred. No. 4; 2e-07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPOSIDMNGATVSNQ 20
DB 133 VPOSIDMNGATVSNQ 142

RESULT 7
US-09-382-685A-4
/ Sequence 5, Application US/09382685A
/ GENERAL INFORMATION:
/ APPLICANT: Myotect, Tracy Lehmanne
/ APPLICANT: Engelhardt, Christian
/ TITLE OF INVENTION: Component of Bromelain
/ FILE REFERENCE: 0621.0750001
/ CURRENT FILING DATE: 1999-08-25
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: PCT/GB98/00591
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9704552.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 4
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-382-685A-4
Query Match 89.5%; Score 94; DB 17; Length 20;
Match Local Similarity 90.0%; Pred. No. 2; 1e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPOSIDMNGATVSNQ 20
DB 1 VPOSIDMNGATVSNQ 20

RESULT 8
US-09-382-685-5
/ Sequence 5, Application US/09382685A
/ GENERAL INFORMATION:
/ APPLICANT: Myotect, Tracy Lehmanne
/ APPLICANT: Engelhardt, Christian
/ TITLE OF INVENTION: Component of Bromelain
/ FILE REFERENCE: 0621.0750001
/ CURRENT FILING DATE: 1999-08-25
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: PCT/GB98/00591
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9704552.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 5
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-382-688-5
Query Match 89.5%; Score 94; DB 17; Length 20;
Match Local Similarity 90.0%; Pred. No. 2; 1e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPOSIDMNGATVSNQ 20
DB 1 VPOSIDMNGATVSNQ 20

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/ TITLE OF INVENTION: Component of Bromelain
/ FILE REFERENCE: US/09791537
/ GENERAL INFORMATION:
/ APPLICANT: Biocrom, Inc.
/ APPLICANT: Denzer, Joseph
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
/ FILE REFERENCE: US/09791537
/ CURRENT FILING DATE: 1999-08-25
/ PRIOR FILING DATE: 1998-02-28
/ PRIOR APPLICATION NUMBER: GB 9704552.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9704552.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 5
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-382-688-5
Query Match 89.5%; Score 94; DB 17; Length 20;
Match Local Similarity 90.0%; Pred. No. 2; 1e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPOSIDMNGATVSNQ 20
DB 1 VPOSIDMNGATVSNQ 20

RESULT 9
US-09-750-210A-5
/ Sequence 5, Application US/09750210A
/ GENERAL INFORMATION:
/ APPLICANT: Myotect, Tracy Lehmanne
/ APPLICANT: Engelhardt, Christian
/ TITLE OF INVENTION: Component of Bromelain
/ FILE REFERENCE: 0621.0746001
/ CURRENT FILING DATE: 2000-12-28
/ PRIOR FILING DATE: 1998-02-28
/ PRIOR APPLICATION NUMBER: US 09/382,688
/ PRIOR FILING DATE: 1998-02-28
/ PRIOR APPLICATION NUMBER: GB 9706119.6
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9704552.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 5
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-750-210A-5
Query Match 88.5%; Score 94; DB 21; Length 20;
Match Local Similarity 89.0%; Pred. No. 4; 1e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPOSIDMNGATVSNQ 20
DB 1 VPOSIDMNGATVSNQ 20

RESULT 10
US-09-674-738-1

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; Sequence 1, Application US/09674738
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: Use of Bromelain Processes for Inhibiting Blood
 ; TITLE OF INVENTION: Coagulation
 ; CURRENT FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: US/09/674,738
 ; CURRENT FILING DATE: 2000-10-31
 ; PRIOR APPLICATION NUMBER: PCT/EP99/04406
 ; NUMBER OF SEQ ID NOS: 2-15
 ; SOFTWARE: Patent Ver. 2.1
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: Bromelain
 ; ORGANISM: Ananas comosus
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: Ananas comosus
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: Ananas comosus

Query Match 88.4%, Score 93; DB 17; Length 20;
 Best Local Similarity 94.7%; Pred. No. 3,2e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPQSDIMWDSGAVTSVQ 19

Db 1 VPQSDIMWDSGAVTSVQ 19

RESULT 11
 US-09-382-688-2

; Sequence 2, Application US/09382688A
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: Use of Bromelain
 ; TITLE OF INVENTION: Coagulation
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; TITLE OF INVENTION: Component of Bromelain
 ; CURRENT FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: US/09/382,688A
 ; CURRENT FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP99/00591
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: GB 9706119.6
 ; PRIOR FILING DATE: 1997-02-28
 ; PRIOR APPLICATION NUMBER: GB 9704252.7
 ; PRIOR FILING DATE: 1997-02-28
 ; PRIOR APPLICATION NUMBER: GB 9703850.9
 ; PRIOR FILING DATE: 1997-02-25
 ; PRIOR APPLICATION NUMBER: GB 9703827.7
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 2
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: Bromelain
 ; ORGANISM: Ananas comosus
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: Ananas comosus

Query Match 88.4%, Score 93; DB 17; Length 21;
 Best Local Similarity 94.7%; Pred. No. 3,2e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPQSDIMWDSGAVTSVQ 19

Db 2 VPQSDIMWDSGAVTSVQ 20

RESULT 12

US-09-382-688-3
 ; Sequence 3, Application US/09382688A
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: Use of Bromelain
 ; TITLE OF INVENTION: Coagulation
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; TITLE OF INVENTION: Component of Bromelain

; FILE REFERENCE: 0623.0740001
 ; CURRENT APPLICATION NUMBER: US/09/382,688A
 ; CURRENT FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP99/00590
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: GB 9706119.6
 ; PRIOR FILING DATE: 1997-02-28
 ; PRIOR APPLICATION NUMBER: GB 9704252.7
 ; PRIOR FILING DATE: 1997-02-28
 ; PRIOR APPLICATION NUMBER: GB 9703850.9
 ; PRIOR FILING DATE: 1997-02-25
 ; PRIOR APPLICATION NUMBER: GB 9703827.7
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 3
 ; TYPE: PRT
 ; LENGTH: 21
 ; ORGANISM: Ananas comosus
 ; TYPE: PRT
 ; LENGTH: 21
 ; ORGANISM: Ananas comosus

Query Match 88.4%, Score 93; DB 17; Length 21;
 Best Local Similarity 94.7%; Pred. No. 3,2e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPQSDIMWDSGAVTSVQ 19

Db 2 VPQSDIMWDSGAVTSVQ 20

RESULT 13

US-09-750-210A-3
 ; Sequence 4, Application US/09750210A
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: Use of Bromelain
 ; TITLE OF INVENTION: Coagulation
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; APPLICANT: Wyrost, Tracy Lehman
 ; TITLE OF INVENTION: Component of Bromelain
 ; CURRENT FILING DATE: 2000-12-29
 ; PRIOR APPLICATION NUMBER: US/09/750,210A
 ; CURRENT FILING DATE: 2000-12-29
 ; PRIOR APPLICATION NUMBER: PCT/GB98/00590
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: GB 9706119.6
 ; PRIOR FILING DATE: 1997-03-25
 ; PRIOR APPLICATION NUMBER: GB 9704252.7
 ; PRIOR FILING DATE: 1997-02-25
 ; PRIOR APPLICATION NUMBER: GB 9703850.9
 ; PRIOR FILING DATE: 1997-02-25
 ; PRIOR APPLICATION NUMBER: GB 9703827.7
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 5
 ; TYPE: PRT
 ; LENGTH: 21
 ; ORGANISM: Ananas comosus
 ; TYPE: PRT
 ; LENGTH: 21
 ; ORGANISM: Ananas comosus

Query Match 88.4%, Score 93; DB 21; Length 21;
 Best Local Similarity 94.7%; Pred. No. 3,2e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPQSDIMWDSGAVTSVQ 19

Db 2 VPQSDIMWDSGAVTSVQ 20

RESULT 14

US-09-750-210A-3
 ; Sequence 5, Application US/08244796

GENERAL INFORMATION:
 APPLICANT: ANDREW R. MILNER, MICHAEL PANICCO, TERENCE W.
 TITLE OF INVENTION: LIVER TUMOR VACCINE AND POLYPEPTIDES USEFUL FOR SAME
 NAMES OF INVENTORS: ANDREW R. MILNER, MICHAEL PANICCO, TERENCE W.
 CORRESPONDENCE ADDRESS:
 ADDRESSES: SCULLY SCOTT McPHER & PRESSER
 10000 RIVERCHASE DRIVE, SUITE 100
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 11330-0299
 COMPUTER READABLE FORM:
 MEDIA TYPE: floppy disk
 COMPUTER FILE NAME: 09-674-738-2.12pm
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: French Release 81.0, Version 81.25
 CURRENT FILING DATE: 08/24/96
 APPLICATION NUMBER: US/08/244,796
 FILING DATE: 15-AUG-1994
 PRIOR APPLICATION DATA: AU P/2109
 APPLICATION NUMBER: PCT/AU94/00051
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGITAL, FRANK
 REGISTRATION NUMBER: 1,946
 TELEPHONE: (1516) 742-4443
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (1516) 742-4443
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 212 amino acids
 TYPE: amino acids
 STRANDNESS: single
 TOPOLOGY: linear
 MODIFIED RESIDUES:
 US-08-244-796-15

Query 1
 1 VPQSDWDSGATVSVD 19
 DB 124 VPQSDWDSGATVSVD 142
 Search completed November 21, 2002, 16:15:43
 CPU time: 138.5 secs

Query Match 88.6% Score 93, DB 21, Length 212,
 Best Local Similarity 94.7%, Pred. No. 4e-06,
 Matches 18, Conservative 0, Mismatches 1, Indels 0,
 Gaps 0,
 DB 2 VPQSDWDSGATVSVD 20

Query Match 88.6% Score 93, DB 21, Length 212,
 Best Local Similarity 94.7%, Pred. No. 4e-06,
 Matches 18, Conservative 0, Mismatches 1, Indels 0,
 Gaps 0,
 DB 2 VPQSDWDSGATVSVD 20

RESULT 15

US-09-791-537-84879
 US-09-791-537-84879 Application US/09/5537

GENERAL INFORMATION:
 APPLICANT: Biogenex, Inc.
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 APPLICANT: DAMEL JOSEPH
 FILING DATE: 06/12/00
 CURRENT FILING DATE: 06/12/00
 CURRENT FILING DATE: 06/12/00
 SOFTWARE: Patent version 3.0
 SEQ ID NO 84879
 TYPE: PRT
 ORGANISM: Acanthamoeba

Query Match 88.6% Score 93, DB 21, Length 156,
 Best Local Similarity 94.7%, Pred. No. 7e-06,
 Matches 18, Conservative 0, Mismatches 1, Indels 0,
 Gaps 0,

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

Copyright (c) 1993 - 2002 CompuGen Ltd

OM protein - protein search, using sw model

Run on: November 21, 2002, 16:09:09 ; Search time 0 Second

86.116 Million cell updates/sec

Title: US-09-674-738-1

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      EVIDENCE SCORE!    100
Sequence:              1 VPSIDWRDYGAVTSVKNN 20

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Gapop 10.0 , Gapexc 0.5

Searched: 99223 begu, 34446456 resi

Total number of hits satisfying chosen parameter

Minimum DE set length: 0

Maximum DB seq length: 2

Post-processing: Minimum Match of

Maximum Macch 10
Listing first 45

Database : Reading Parents As New :

1: /cgn2_6/prod/ta71/paa/f

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3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.rep;
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4: /cgn2_6/prodata/1/pae/US08_NEW_CONB.pcp:
5: /cgn2_6/prodata/1/pae/US09_NEW_CONB.pcp:
6: /cgn2_6/prodata/1/pae/US10_NEW_CONB.pcp:
7: /cgn2_6/prodata/1/pae/US60_NEW_CONB.pcp:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	70	230	US-09-724-676-80619	Sequence 8013.9
3	70	230	US-09-724-676-80619	Sequence 8013.9
4	70	230	US-09-724-676-80619	Sequence 8013.9
5	70	230	US-09-724-676-80619	Sequence 8013.9
6	70	230	US-09-724-676-80619	Sequence 8013.9
7	70	230	US-09-724-676-80619	Sequence 8013.9
8	70	230	US-09-724-676-80619	Sequence 8013.9
9	70	230	US-09-724-676-80619	Sequence 8013.9
10	70	230	US-09-724-676-80619	Sequence 8013.9
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12	70	230	US-09-724-676-80619	Sequence 8013.9
13	70	230	US-09-724-676-80619	Sequence 8013.9
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15	70	230	US-09-724-676-80619	Sequence 8013.9
16	70	230	US-09-724-676-80619	Sequence 8013.9
17	70	230	US-09-724-676-80619	Sequence 8013.9
18	70	230	US-09-724-676-80619	Sequence 8013.9
19	70	230	US-09-724-676-80619	Sequence 8013.9
20	70	230	US-09-724-676-80619	Sequence 8013.9
21	70	230	US-09-724-676-80619	Sequence 8013.9
22	70	230	US-09-724-676-80619	Sequence 8013.9
23	70	230	US-09-724-676-80619	Sequence 8013.9
24	70	230	US-09-724-676-80619	Sequence 8013.9
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46	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80591
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53	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80598
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59	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80604
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62	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80607
63	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80608
64	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80609
65	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80610
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68	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80613
69	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80614
70	65	63.9	233.0	US	0	-72.8	65.0	80.0	Sequence	80615</

RESULT 1
 1. Sequence: 606.64619
 2. Species: 90619
 3. ABBREVIATION: application US/0972676
 4. APPLICANT INFORMATION
 5. APPLICANT: Compugen LTD
 6. FILL DATE: 2000-11-28
 7. FILL REFERENCE: 125815 Applicant
 8. CURRENT APPLICATION NUMBER: US/0972676
 9. CURRENT FILING DATE: 2000-11-28
 10. INVENTOR: 90619
 11. SOFTWARE: Patent version 3.2
 12. SEQ ID NO 90619
 13. LENGTH: 230
 14. ORGANISM: Homo sapiens
 15. ORGANISM: Homo sapiens
 16. 09-724-676-0619

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Query Match      64.8%; Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0
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DD 115 URSWINGCVCATTWAYD 133

RESULT 2
US-09-724-676-80020
Sequence 80520 Application US/0974676
Applicant: Compasid LTD
Title Of Invention Variants of alternative splicing
Current Application Number US/09724,676
Current Filing Date: 2000-11-28
Number Of SEQ IN: 9722
Number Of SEQ OUT IN Version: 3,2
SEQ ID NO 80520
LENGTH: 230
CARBONISM: Homo sapiens
US-09-724-676-80020

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OY      1  WFOSIDMDRYGATSYVKQ  19
      : : : : : : : : : : : : : : :
Query Match      Score 70: DB 5: Length 210:
Best Local Similarity 63.4%:
Pred. No. 0.00065:
Matches 12: Conservative 4: Mismatches 3: Indels 0: Gaps 0

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Db 115 LPSVDMREKGVTFVFNQ 133
RESULT 3
US-09-724-676-80621
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-09-724-676-80621
; ORGANISM: Homo sapiens
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patent version 3.2
; SEQ ID NO 80621
; TYPE: PRT
; LENGTH: 230
; ORGANISM: Homo sapiens
US-09-724-676-80621
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Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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Db 115 LPSVDMREKGVTFVFNQ 133
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US-09-724-674-80622
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Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-09-724-674-80622
; ORGANISM: Homo sapiens
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patent version 3.2
; SEQ ID NO 80622
; TYPE: PRT
; LENGTH: 230
; ORGANISM: Homo sapiens
US-09-724-674-80622
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
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QY 1 VPOSIDMRGVATVFNQ 19
Db 115 LPSVDMREKGVTFVFNQ 133
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US-09-724-676-80624
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Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-09-724-676-80624
; ORGANISM: Homo sapiens
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patent version 3.2
; SEQ ID NO 80624
; TYPE: PRT
; LENGTH: 230
; ORGANISM: Homo sapiens
US-09-724-676-80624
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPOSIDMRGVATVFNQ 19
Db 115 LPSVDMREKGVTFVFNQ 133
RESULT 6
US-09-724-676-80625
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Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-09-724-676-80625
; ORGANISM: Homo sapiens
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patent version 3.2
; SEQ ID NO 80625
; TYPE: PRT
; LENGTH: 230
; ORGANISM: Homo sapiens
US-09-724-676-80625
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPOSIDMRGVATVFNQ 19
Db 115 LPSVDMREKGVTFVFNQ 133
RESULT 7
US-09-724-676-80626
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-09-724-676-80626
; ORGANISM: Homo sapiens
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patent version 3.2
; SEQ ID NO 80626
; TYPE: PRT
; LENGTH: 230
; ORGANISM: Homo sapiens
US-09-724-676-80626
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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Db 115 LPSVDMREKGVTFVFNQ 133
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US-09-724-676-80627
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Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-09-724-676-80627
; ORGANISM: Homo sapiens
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: Patent version 3.2
; SEQ ID NO 80627
; TYPE: PRT
; LENGTH: 230
; ORGANISM: Homo sapiens
US-09-724-676-80627
Query Match 64.8% Score 70; DB 5; Length 230;
Best Local Similarity 63.2%; Pred. No. 0.00045;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPOSIDMRGVATVFNQ 19
Db 115 LPSVDMREKGVTFVFNQ 133

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: GENERAL INFORMATION:
:   TITLE OF INVENTION: Variants of alternative splicing
:   FILE REFERENCE: 129181.4 CompuGen
:   CURRENT APPLICATION NUMBER: US/09/724,676
:   CURRENT FILING DATE: 2000-11-28
:   NUMBER OF SEQ ID NOS: 97222
:   SOFTWARE: PatentIn version 3.2
:   SEQ ID NO: 80586
:   SEQ ID NO: 80587
:   SEQ ID NO: 80588
:   TYPE: PAT
: ORGANISM: Homo sapiens
: US-09-724,676-80588

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Best local Similarity 63.2%;
Pred. No. 0.00049;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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DB      115 LPSVOMREKGVYTPVNO 113

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RESULT 15
US-02-724-676-80659
: Sequence 80589, Application US/024676
: INVENTOR: JAMES L. HANCOCK
: APPLICANT: Computer LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181 Computer
: FILING DATE: 2000-11-28
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: PRIORITY: 129181
: SEQ ID NO 80589
: LENGTH: 250
: TYPE: PRT
: ORIGIN: Homo sapiens
US-02-724-676-80593

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Query Match      64.8%  Score 70; DB 5; Length 250;
Best Local Similarity 63.2%;  Pred.No. 0.00049;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 VFQSDWRYDYGATVSNQ 19
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DB     115 LPSVQWREKGYVTVNQ 131

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Search completed: November 21, 2002, 16:16:04
Job time : 8 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OK protein - protein search, using ew model

Run on: November 21, 2002, 16:10:04 Search time 7 seconds

(without alignments)
44,747 Million cell updates/sec

Title: US-09-674-738-1

Sequence: 1 VP03IMDQVATVSYXNN 20

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Gapop 10.0, Gapexp 0.5

Total number of hits satisfying chosen parameters: 10480

Minimum DB seq length: 800000000

Maximum DB seq length: Minimum Match 0%

Post-processing: Minimum Match 0%

Warning files: 48 summaries

Database:

- 1. Published Applications, AA*
- 2. /cgn2_6/p/cdate/2/pubseq/US05_NSW_PUB_PEP.*
- 3. /cgn2_6/p/cdate/2/pubseq/US05_NSW_PUB_PEP.*
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- 13. /cgn2_6/p/cdate/2/pubseq/US05_NSW_PUB_PEP.*
- 14. /cgn2_6/p/cdate/2/pubseq/US05_NSW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMILARITIES

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2	89.8	20	10	US-09-750-210A-3	Sequence 1, Appl 1
3	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
4	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
5	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
6	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
7	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
8	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
9	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
10	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
11	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
12	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
13	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
14	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
15	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
16	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
17	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1
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20	86.1	20	10	US-09-750-210A-3	Sequence 1, Appl 1

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21	49.5	45.8	33.5	12	US-10-114-464-10	Sequence 10, Appl 1
22	49.5	45.8	33.5	12	US-10-114-464-10	Sequence 10, Appl 1
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ALIGNMENTS

RESULT 1
US-09-750-210A-3
Sequence 1, Application US/09750210A
GENERAL INFORMATION: 125011
APPLICANT: Mycot, Tracy Leanne
APPLICANT: Pect, Kelly-Christina
TITLE OF INVENTION: Component of Broomlain
FILE REFERENCE: 0623, 0748001
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: US/09382,688
PRIOR FILING DATE: 1999-02-28/09750210A
PRIOR APPLICATION NUMBER: PCT/GB98/05590
PRIOR FILING DATE: 1997-02-28/9703856,9
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: GB 9703827,7
SOFTWARE: Patent, Ver. 2.0
SEQ ID NO: 3
TYPE: PAT
ORGANISM: ORGANISM: Annas comoue
US-09-750-210A-3
Query Match: 100.0%; Score 108; DB 10; Length 21;
Best Local Similarity: 100.0%; Pct 108; DB 10;
Matches: 20; Conservative: 0; Mismatches: 0; Indels: 0; Caps: 0;
Cy: 1 VP03IMDQVATVSYXNN 20
DB: 2 VP03IMDQVATVSYXNN 21
RESULT 2

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US-09-750-210A-5
/ Sequence 1, Application US/09750210A
/ Patent No. US2002010225A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyott, Tracy Lehane
/ APPLICANT: Engwerda, Christian
/ APPLICANT: Peek, Keith
/ TITLE OF INVENTION: Component of Bromelain
/ CURRENT FILING DATE: 2000-12-29
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR FILING DATE: 1995-08-25
/ PRIOR APPLICATION NUMBER: US/09/750,210A
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR FILING DATE: 1995-08-25
/ PRIOR APPLICATION NUMBER: GB 9704252.7
/ PRIOR APPLICATION NUMBER: GB 9706119.6
/ PRIOR APPLICATION NUMBER: GB 9704252.7
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ PRIOR FILING DATE: 1997-02-25
/ PRIOR FILING DATE: 1997-02-25
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 20
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-750-210A-5

Query Match
Best Local Similarity 89.94; Score 97; DB 10; Length 20;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VP0SDMDRGVTSVNNQ 19
DB 1 VP0SDMDRGVTSVNNQ 19

US-09-750-210A-4
/ Sequence 1, Application US/09750210A
/ Patent No. US2002010225A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyott, Tracy Lehane
/ APPLICANT: Engwerda, Christian
/ APPLICANT: Peek, Keith
/ TITLE OF INVENTION: Component of Bromelain
/ CURRENT FILING DATE: 2000-12-29
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR FILING DATE: 1995-08-25
/ PRIOR APPLICATION NUMBER: PCT/GB98/00590
/ PRIOR APPLICATION NUMBER: GB 9704252.7
/ PRIOR APPLICATION NUMBER: GB 9706119.6
/ PRIOR APPLICATION NUMBER: GB 9704252.7
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ PRIOR FILING DATE: 1997-02-25
/ PRIOR FILING DATE: 1997-02-25
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 2
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-750-210A-2

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Best Local Similarity 81.94; Score 88; DB 10; Length 18;
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OY 1 VP0SDMDRGVTSVNN 18
DB 1 VP0SDMDRGVTSVNN 18

US-09-750-210A-1
/ Sequence 1, Application US/09750210A
/ Patent No. US2002010225A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyott, Tracy Lehane
/ APPLICANT: Engwerda, Christian
/ APPLICANT: Peek, Keith
/ TITLE OF INVENTION: Component of Bromelain
/ CURRENT FILING DATE: 2000-12-29
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR FILING DATE: 1995-08-25
/ PRIOR APPLICATION NUMBER: US/09/750,210A
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR FILING DATE: 1995-08-25
/ PRIOR APPLICATION NUMBER: PCT/GB98/00590
/ PRIOR APPLICATION NUMBER: GB 9706119.6
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/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ PRIOR FILING DATE: 1997-02-28
/ PRIOR APPLICATION NUMBER: GB 9703827.7
/ PRIOR FILING DATE: 1997-02-25
/ NUMBER OF SEQ ID NOS: 5
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/ SEQ ID NO: 20
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Ananas comosus
US-09-750-210A-1

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NUMBERS OF SEQ ID NOS: 5
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
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 TYPE: PRT
 ORGANISM: ORGANISM: Anas carolinensis
 US-09-750-210A-1

Query Match 63.7% Score 71; DB 10; Length 21;
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 Matches 11; Conservative 2; Mismatches 4; Indels 0;
 Gaps 0;

1 VP05IMDQVATSVVNO 19
 2 VP05IMDQVATSVVNO 20

RESULT 4
 US-09-462-846-3
 Sequence 3, Application US/09462846

PATENT NO. US2002031807A1
 INVENTOR: BACILLUS, et al.
 APPLICANT: BACILLUS, et al.
 TITLE OF INVENTION: Processes From Gram-Positive Organisms
 CURRENT APPLICATION NUMBER: US/09/462,846
 PRIOR FILING DATE: 2000-01-13/08/19529
 PRIOR FILING DATE: 1998-07-14
 PRIOR APPLICATION NUMBER: EP 9705227.7
 NUMBER OF SEQ ID NOS: 197-07-15
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Bacillus subtilis

US-09-462-846-3

Query Match 63.7% Score 71; DB 10; Length 20;
 Best Local Similarity 61.2%; Pred. No. 0.00612;
 Matches 12; Conservative 3; Mismatches 4; Indels 0;
 Gaps 0;

1 VP05IMDQVATSVVNO 19
 2 VP05IMDQVATSVVNO 27

RESULT 7
 US-09-953-956-9
 Sequence 9, Application US/09953956
 PATENT NO. US200203117A1
 INVENTOR: HARTING, et al.
 APPLICANT: HARTING, et al.
 TITLE OF INVENTION: OSTEOLYST-DERIVED CATHETERIN
 CURRENT APPLICATION NUMBER: US/09/953,956
 PRIOR FILING DATE: 1998-12-23
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 09/219,441
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 333
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-953-956-9

Query Match 63.4% Score 69; DB 10; Length 333;
 Best Local Similarity 66.7%; Pred. No. 0.00041;
 Matches 12; Conservative 3; Mismatches 3; Indels 0;
 Gaps 0;

2 POSIMRWGVATSVVNO 19

US-10-114-464-9
 Sequence 9, Application US/10114464

PATENT NO. US2002014246A1
 INVENTOR: HARTING, et al.
 APPLICANT: HARTING, et al.
 TITLE OF INVENTION: OSTEOLYST-DERIVED CATHETERIN
 CURRENT APPLICATION NUMBER: US/10/114,464
 PRIOR FILING DATE: 2002-04-03/04/53,125
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 08/208,007
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 333
 LENGTH: 333
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-114-464-9

US-10-114-464-9

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1 POSIMRWGVATSVVNO 19
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US-09-529-063-1
 Sequence 9, Application US/09529063

PATENT NO. US2002010542A1
 INVENTOR: SHIMADA, SHIGEH
 APPLICANT: SHIMADA, SHIGEH
 TITLE OF INVENTION: POLYMERIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
 CURRENT APPLICATION NUMBER: US/09/529,063
 PRIOR FILING DATE: 1998-10-06
 PRIOR FILING DATE: 1997-10-07
 PRIOR APPLICATION NUMBER: PCT/JP98/04514
 NUMBER OF SEQ ID NOS: 117
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 334
 LENGTH: 334
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-529-063-1

US-09-529-063-1

Query Match 63.4% Score 67; DB 10; Length 334;
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US-09-529-063-1

US-09-529-063-1

US-09-529-063-1
 Sequence 2, Application US/0990064
 Patent No. US2002016475A1


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US-09-953-956-2
/ Sequence 2, Application US/09953956
/ GENERAL INFORMATION:
/   APPLICATION: 10791
/   APPLICANT: Haering, et al
/   TITLE OF INVENTION: OXAL OSTEOLAST-DERIVED CATHEPSIN
/   FILING DATE: 1998-12-23
/   CURRENT FILING DATE: 2001-09-18
/   PRIORITY DATE: 1998-12-23
/   NUMBER OF SEQ ID NOS: 14
/   SOFTWARE: Patent Ver. 2.1
/   LENGTH: 329
/   TYPE: PAT
/   ORGANISM: Homo sapiens
US-09-953-956-2
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Match: 11; Similarity: 51.11; Percent: 0.577;
Matches: 2; Mismatches: 5; Indels: 0; Gaps: 0;
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DB 116 PSVDYRKQVTVVNO 133

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Search completed: November 21, 2002, 16:16:25
 Job time : 7 secs



Genome version 5.1.3
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ON protein - protein search, using sw method

Run on: November 21, 2002, 16:10:04 (Search time 5 seconds)

(without alignments) 44,747 Million cell updates/sec

Title: US-09-674-738-2

Perfect score: 100%IDMSDQATYVIND 30

Sequence: 1

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Total number of hits against chosen parameters: 10460

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing files to summarize

Database: Published Applications A1.*
1. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*
2. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*
3. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*
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6. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*
7. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*
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13. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*
14. /cgn2_6/pdata/2/pubpa/US06_NSW_PIB.ppi.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHOWBITS

Result No.	Score	Match	Length	DB ID	Description
1	105	100.0	20	US-09-750-210A-4	Sequence 4, App1
2	93	86.6	21	US-09-750-210A-3	Sequence 3, App1
3	78	75.2	18	US-09-750-210A-2	Sequence 2, App1
4	78	75.2	18	US-09-750-210A-1	Sequence 1, App1
5	75	72.8	16	US-09-482-846-1	Sequence 1, App1
6	75	72.8	16	US-09-482-846-2	Sequence 2, App1
7	77	73.3	13	US-09-953-956-9	Sequence 9, App1
8	77	73.3	13	US-09-953-956-8	Sequence 8, App1
9	77	73.3	13	US-09-953-956-7	Sequence 7, App1
10	72	68.6	11	US-10-124-464-8	Sequence 8, App1
11	72	68.6	11	US-10-124-464-7	Sequence 7, App1
12	72	68.6	11	US-10-124-464-6	Sequence 6, App1
13	65	61.9	12	US-09-953-956-7	Sequence 7, App1
14	65	61.9	12	US-09-953-956-8	Sequence 8, App1
15	64	61.0	10	US-09-953-956-9	Sequence 9, App1
16	64	61.0	10	US-09-953-956-8	Sequence 8, App1
17	64	61.0	10	US-09-953-956-7	Sequence 7, App1
18	57.5	54.8	12	US-09-953-956-10	Sequence 10, App1

20	57.5	54.8	364	10	US-09-925-302-478	Sequence 778, App
21	57.5	54.3	337	10	US-09-925-301-1221	Sequence 1021, App
22	57.5	54.3	337	10	US-09-925-301-1107	Sequence 1107, App
23	44.4	41.3	565	10	US-09-925-301-1107	Sequence 1107, App
24	43	41.0	119	10	US-09-881-243-1545	Sequence 1043, App
25	43	41.0	1247	10	US-09-881-243-1545	Sequence 1043, App
26	43	41.0	1247	10	US-09-881-243-1545	Sequence 1043, App
27	42	40.0	185	10	US-09-881-237-7811	Sequence 7811, App1
28	42	40.0	343	10	US-09-881-237-7811	Sequence 7811, App1
29	42	40.0	343	10	US-09-881-237-7811	Sequence 7811, App1
30	42	40.0	574	10	US-09-906-743-6	Sequence 11, App1
31	42	40.0	574	10	US-09-906-743-6	Sequence 11, App1
32	42	40.0	1165	12	US-10-015-768-10	Sequence 10, App1
33	42	40.0	1165	12	US-10-015-768-10	Sequence 10, App1
34	42	40.0	1165	12	US-10-015-768-10	Sequence 10, App1
35	41	39.0	190	10	US-09-811-284-272	Sequence 272, App
36	41	39.0	190	10	US-09-811-284-272	Sequence 272, App
37	41	39.0	127	10	US-09-731-973-101	Sequence 101, App
38	41	39.0	516	10	US-09-971-611-23	Sequence 101, App
39	40.5	38.6	472	10	US-09-860-728-130	Sequence 130, App1
40	40.5	38.6	472	10	US-09-860-728-130	Sequence 130, App1
41	39.5	37.6	806	10	US-09-925-217-1117	Sequence 1117, App
42	39.5	37.6	806	10	US-09-925-217-1117	Sequence 1117, App
43	39	37.1	637	10	US-09-815-943-1666	Sequence 1366, App
44	39	37.1	637	10	US-09-815-943-1666	Sequence 1366, App
45	39	37.1	637	10	US-09-862-007-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-750-210A-4
Sequence 4, Application US-09750210A
US-09-750-210A-4
Sequence 4, Application US-09750210A
GENERAL INFORMATION:
APPLICANT: Myocet, Tracy Lehman
APPLICANT: Beck, Keith
TITLE OF INVENTION: Component of Bromelain
FILE REFERENCE: 0021 (PDB) US-09750-210A
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: US 09/182,688
PRIOR APPLICATION NUMBER: PCT/GB99/00590
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1997-02-28
PRIOR FILING DATE: 1997-02-25
PRIOR APPLICATION NUMBER: GB 970432.7
PRIOR APPLICATION NUMBER: GB 970432.7
NUMBER OF SEQ. RES: 199-02-25
SOFTWARE: Patented Ver. 2.0
SEQ ID NO: 4
TYPE: PRT
ORGANISM: ORKINUS: Anna Comas
US-09-750-210A-4
Query Seq: 100.0%, Pctd No. 1,861,17
Best Local Similarity 100.0%, Pctd No. 1,861,17
Matches: 20, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0,
DB 1 VS09IDMSDQATYVIND 20
RESULT 2


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NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ SEQUENCE: 1
/ TYPE: PRT
/ ORGANISM: ORGANISM: Annas comus
US-09-750-2100-1
Query Match: 75.2%, Score 79; DB 10; Length 21;
Best Local Similarity: 70.0%; Pred. No. 19e-07;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 VP01WDMGCAVTVNMG 20
Db 2 LP01WDMGCAVTVNMG 21

RESULT 6
US-09-452-846-3
/ Sequence 3, Application US/09462846
/ Patent No. US6002014448A1
/ GENERAL INFORMATION:
/ APPLICANT: Eschall, David A.
/ INVENTOR: Eschall, David A.
/ TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHERSIN
/ FILE REFERENCE: PTO7021
/ CURRENT APPLICATION NUMBER: US/09/462,846
/ CURRENT FILING DATE: 2000-01-11/058/19529
/ PRIOR FILING DATE: 1998-07-14
/ PRIOR APPLICATION NUMBER: EP 93105227.7
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FASTSD For Windows Version 3.10
/ SEQ ID NO 3
/ TYPE: PRT
/ LENGTH: 320
/ ORGANISM: Bacillus subtilis
US-09-743-846-3
Query Match: 75.2%, Score 79; DB 10; Length 220;
Best Local Similarity: 66.4%; Pred. No. 5.5e-04;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 VP01WDMGCAVTVNMG 20
Db 9 IFP01WDMGCAVTVNMG 28

RESULT 7
US-09-953-956-9
/ Sequence 9, Application US/09933956
/ Patent No. US6002014448A1
/ GENERAL INFORMATION:
/ APPLICANT: Hastings, et al.
/ INVENTOR: Hastings, et al.
/ TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHERSIN
/ FILE REFERENCE: PTO7021
/ CURRENT APPLICATION NUMBER: US/09/953,956
/ CURRENT FILING DATE: 2001-02-18
/ PRIOR FILING DATE: 1998-12-23/218,441
/ PRIOR APPLICATION NUMBER: 09/218,441
/ NUMBER OF SEQ ID NOS: 14
/ SEQ ID NO 9
/ TYPE: PRT
/ LENGTH: 333
/ ORGANISM: Homo sapiens
US-09-953-956-9
Query Match: 73.3%, Score 77; DB 10; Length 333;
Best Local Similarity: 66.4%; Pred. No. 1.9e-05;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 P01WDMGCAVTVNMG 20

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Db 115 P01WDMGCAVTVNMG 133

RESULT 8
US-10-114-464-3
/ Sequence 8, Application US/10114464
/ Patent No. US6002014448A1
/ GENERAL INFORMATION:
/ APPLICANT: Eschall, David A.
/ INVENTOR: Eschall, David A.
/ TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHERSIN
/ FILE REFERENCE: PTO7021
/ CURRENT APPLICATION NUMBER: US/10/114,464
/ CURRENT FILING DATE: 2001-02-18
/ PRIOR FILING DATE: 1998-11-07
/ PRIOR APPLICATION NUMBER: 09/553,135
/ PRIOR FILING DATE: 1998-03-08
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ TYPE: PRT
/ LENGTH: 333
/ ORGANISM: Homo sapiens
US-10-114-464-3
Query Match: 73.3%, Score 77; DB 10; Length 333;
Best Local Similarity: 66.4%; Pred. No. 1.9e-05;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 P01WDMGCAVTVNMG 20
Db 115 P01WDMGCAVTVNMG 133

RESULT 9
US-09-953-966-8
/ Sequence 9, Application US/09933956
/ Patent No. US6002014448A1
/ GENERAL INFORMATION:
/ APPLICANT: Hastings, et al.
/ INVENTOR: Hastings, et al.
/ TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHERSIN
/ FILE REFERENCE: PTO7021
/ CURRENT APPLICATION NUMBER: US/09/953,956
/ CURRENT FILING DATE: 2001-02-18
/ PRIOR FILING DATE: 1998-12-23
/ PRIOR APPLICATION NUMBER: 09/218,441
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ TYPE: PRT
/ LENGTH: 333
/ ORGANISM: Homo sapiens
US-09-953-956-8
Query Match: 68.0%, Score 72; DB 10; Length 331;
Best Local Similarity: 60.0%; Pred. No. 0.00013;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 VP01WDMGCAVTVNMG 20
Db 115 LP01WDMGCAVTVNMG 134

RESULT 10
US-10-114-464-8
/ Sequence 8, Application US/10114464
/ Patent No. US6002014448A1
/ GENERAL INFORMATION:
/ APPLICANT: Hastings, et al.
/ INVENTOR: Hastings, et al.
/ TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHERSIN
/ FILE REFERENCE: PTO7021
/ CURRENT APPLICATION NUMBER: US/10/114,464
/ CURRENT FILING DATE: 2001-02-18
/ PRIOR FILING DATE: 1998-11-07
/ PRIOR APPLICATION NUMBER: 09/553,135
/ PRIOR FILING DATE: 1998-03-08
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ TYPE: PRT
/ LENGTH: 333
/ ORGANISM: Homo sapiens
US-10-114-464-8
Query Match: 73.3%, Score 77; DB 10; Length 333;
Best Local Similarity: 66.4%; Pred. No. 1.9e-05;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 P01WDMGCAVTVNMG 20

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; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/553,125
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: 08/209,007
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 8 PATENTIN Ver. 2.1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-464-8
Query Match
Best Local Similarity 68.6%; Score 72; DB 12; Length 331;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 VPQSDMRSGATVTKNQ 20
DB 115 LPQSDVMRSGATVTKNQ 134
RESULT 11
US-09-590-064-2
Query Match
Best Local Similarity 60.0%; Score 71; DB 6; Length 331;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 VPQSDMRSGATVTKNQ 20
DB 115 LPQSDVMRSGATVTKNQ 134
RESULT 12
US-09-529-063-1
Query Match
Best Local Similarity 65.7%; Score 69; DB 10; Length 334;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 VPQSDMRSGATVTKNQ 19
DB 114 LPQSDVMRSGATVTKNQ 132
RESULT 13
US-09-953-956-7
Query Match
Best Local Similarity 61.0%; Score 65; DB 10; Length 329;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 2 POSIDMRSGATVTKNQ 20
DB 116 PPSIDYRKGATVTKNQ 134
RESULT 14
US-10-114-464-7
Query Match
Best Local Similarity 61.9%; Score 65; DB 13; Length 329;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 2 POSIDMRSGATVTKNQ 20
DB 116 PPSIDYRKGATVTKNQ 134
RESULT 15
US-10-114-464-7
Query Match
Best Local Similarity 61.9%; Score 65; DB 13; Length 329;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 2 POSIDMRSGATVTKNQ 20
DB 116 PPSIDYRKGATVTKNQ 134

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US-09-953-956-2
/ Sequence 2, Application US/0993956
/ General: US/09/953-2
/ GENERAL INFORMATION:
/ APPLICATION: Hastings, et al.
/ TITLE: OSTEOCLAST-DERIVED CATEPSIN
/ FILING DATE: 1998-12-23
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patentin Ver. 2.1
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-953-956-2
Query Match: 61.04; Score 64; DB 10;
Base local: 24; Pos: 0.025;
Matches: 2; Mismatches: 5; Indels: 0; Gaps: 0;
QY 2 POSITIVE MATCHES: 20
DB 116 POSITIVE MATCHES: 134

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Search completed: November 21, 2002, 16:16:26
 Job time : 8 secs

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